GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 19, 2004, 23:34:06 ; Search time 99 Seconds
(without alignments)
2152.537 Million cell updates/sec

Title: US-09-784-810C-2
Perfect score: 2015
Sequence: 1 MDPAGGPRGVLPRPCRVLVL.....CVEPPPSWKPQQMPPPEEPL 384

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09784810/runat_13082004_091729_20869/app_query.fasta_1.583
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09784810_@CGN_1_1_69_@runat_13082004_091729_20869 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1962	97.4	1155	4	US-09-970-516-1	Sequence 1, Appli
	2	1927	95.6	1533	4	US-09-205-258-90	Sequence 90, Appl
	3	1587.5	78.8	1149	4	US-09-970-516-5	Sequence 5, Appli
	4	856.5	42.5	1857	4	US-09-970-516-3	Sequence 3, Appli
	5	198	9.8	2462	4	US-09-620-312D-796	Sequence 796, App
	6	147.5	7.3	915	4	US-09-134-000C-1961	Sequence 1961, Ap
	7	130	6.5	978	4	US-09-107-532A-3132	Sequence 3132, Ap
	8	127.5	6.3	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	9	126.5	6.3	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	10	125.5	6.2	894	4	US-09-134-000C-211	Sequence 211, App
	11	118.5	5.9	942	4	US-09-107-532A-3500	Sequence 3500, Ap
c	12	113	5.6	900	4	US-08-961-527-332	Sequence 332, App
	13	113	5.6	1035	4	US-09-134-000C-408	Sequence 408, App
c	14	110	5.5	1003	4	US-09-221-017B-1064	Sequence 1064, Ap
c	15	108	5.4	13542	4	US-08-956-171E-154	Sequence 154, App
	16	106.5	5.3	1458	4	US-09-252-991A-14865	Sequence 14865, A
	17	105	5.2	975	4	US-09-134-001C-1937	Sequence 1937, Ap
	18	103.5	5.1	912	4	US-09-107-532A-1479	Sequence 1479, Ap
	19	102.5	5.1	5092	3	US-09-412-545-1	Sequence 1, Appli
	20	101	5.0	1548	4	US-09-252-991A-5880	Sequence 5880, Ap
c	21	99.5	4.9	2493	4	US-09-252-991A-12390	Sequence 12390, A
	22	99.5	4.9	3024	4	US-09-252-991A-12202	Sequence 12202, A
c	23	99.5	4.9	111282	4	US-09-754-250-3	Sequence 3, Appli
	24	98	4.9	22481	4	US-08-367-841A-43	Sequence 43, Appl
	25	98	4.9	22481	5	PCT-US95-07201-43	Sequence 43, Appl
	26	98	4.9	22484	4	US-09-875-223-2	Sequence 2, Appli
	27	98	4.9	22484	4	US-09-875-114-2	Sequence 2, Appli
c	28	98	4.9	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c	29	98	4.9	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	30	97	4.8	1131	4	US-09-252-991A-691	Sequence 691, App
c	31	97	4.8	3054	4	US-09-252-991A-720	Sequence 720, App
	32	97	4.8	6885	4	US-09-252-991A-660	Sequence 660, App
c	33	96.5	4.8	5727	4	US-08-956-171E-190	Sequence 190, App
	34	96	4.8	2657	4	US-09-495-050A-191	Sequence 191, App
	35	96	4.8	23673	4	US-09-773-816-1	Sequence 1, Appli
c	36	95	4.7	1800	4	US-09-252-991A-12496	Sequence 12496, A
c	37	95	4.7	1956	4	US-09-252-991A-9165	Sequence 9165, Ap
c	38	95	4.7	36519	3	US-08-923-137-2	Sequence 2, Appli
	39	94.5	4.7	1851	4	US-09-252-991A-9067	Sequence 9067, Ap
c	40	94.5	4.7	2849	4	US-09-866-028-77	Sequence 77, Appl
c	41	94.5	4.7	3681	4	US-09-581-105-1	Sequence 1, Appli
	42	94	4.7	1617	4	US-09-252-991A-8802	Sequence 8802, Ap
c	43	94	4.7	1649	2	US-08-845-566-2	Sequence 2, Appli
c	44	94	4.7	2416	4	US-09-016-434-1058	Sequence 1058, Ap
c	45	94	4.7	536165	4	US-09-214-808-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-970-516-1
; Sequence 1, Application US/09970516
; Patent No. 6610534
; GENERAL INFORMATION:
; APPLICANT: No. 6610534artis AG
; TITLE OF INVENTION: Induction of blood vessel formation through administration of
; TITLE OF INVENTION: polynucleotides encoding sphingosine kinases
; FILE REFERENCE: 4-31617
; CURRENT APPLICATION NUMBER: US/09/970,516
; CURRENT FILING DATE: 2001-10-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1155)
; OTHER INFORMATION:
US-09-970-516-1

Alignment Scores:

Pred. No.:	1.54e-218	Length:	1155
Score:	1962.00	Matches:	375
Percent Similarity:	98.18%	Conservative:	2
Best Local Similarity:	97.66%	Mismatches:	7
Query Match:	97.37%	Indels:	0
DB:	4	Gaps:	0

US-09-784-810C-2 (1-384) x US-09-970-516-1 (1-1155)

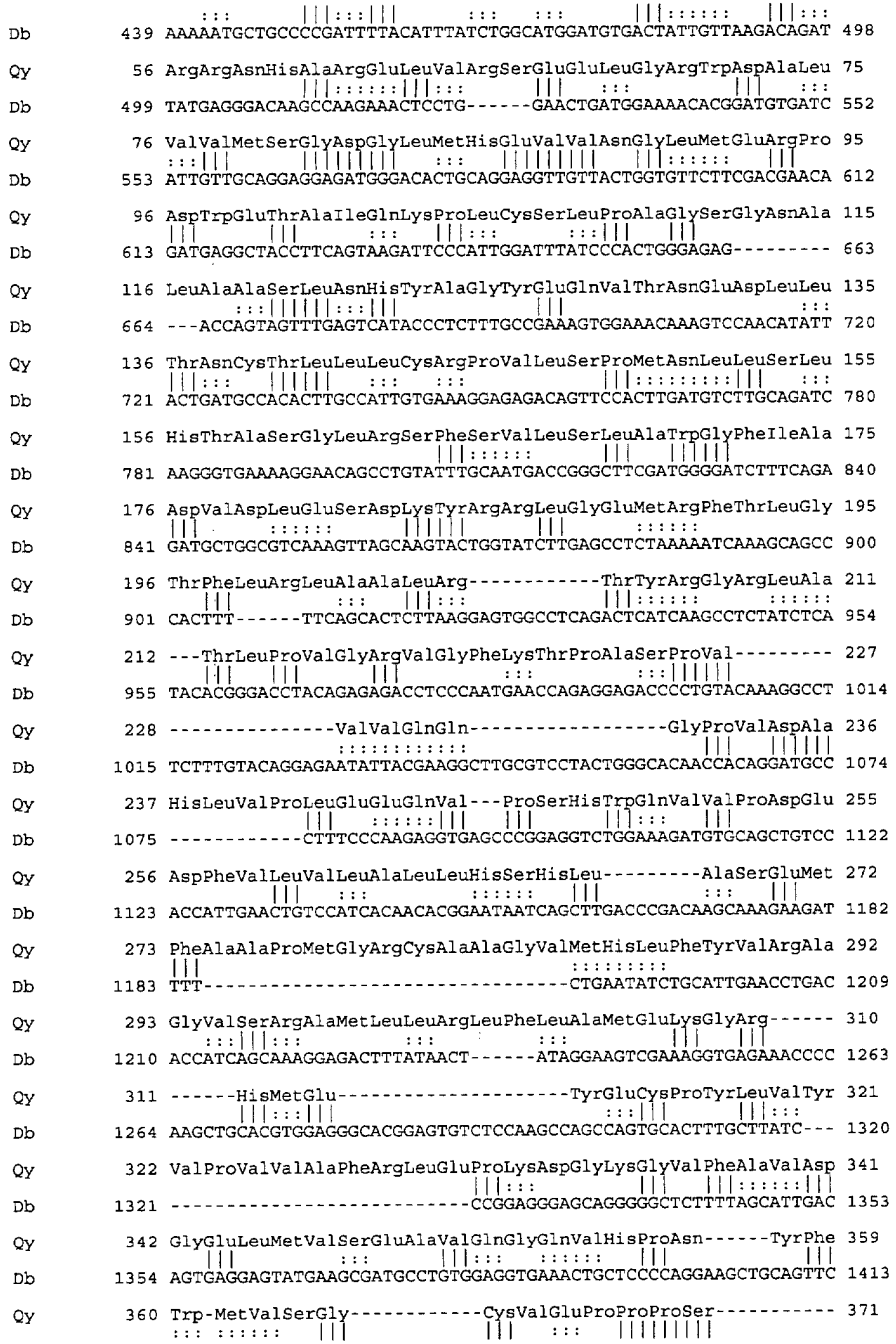
```
Qy          1 MetAspProAlaGlyGlyProArgGlyValLeuProArgProCysArgValLeuValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGATCCAGCGGGCGGCCCCCGGGGCGTGCTCCCGCGGCCCTGCCGCGTGCTGGTGCTG 60
```

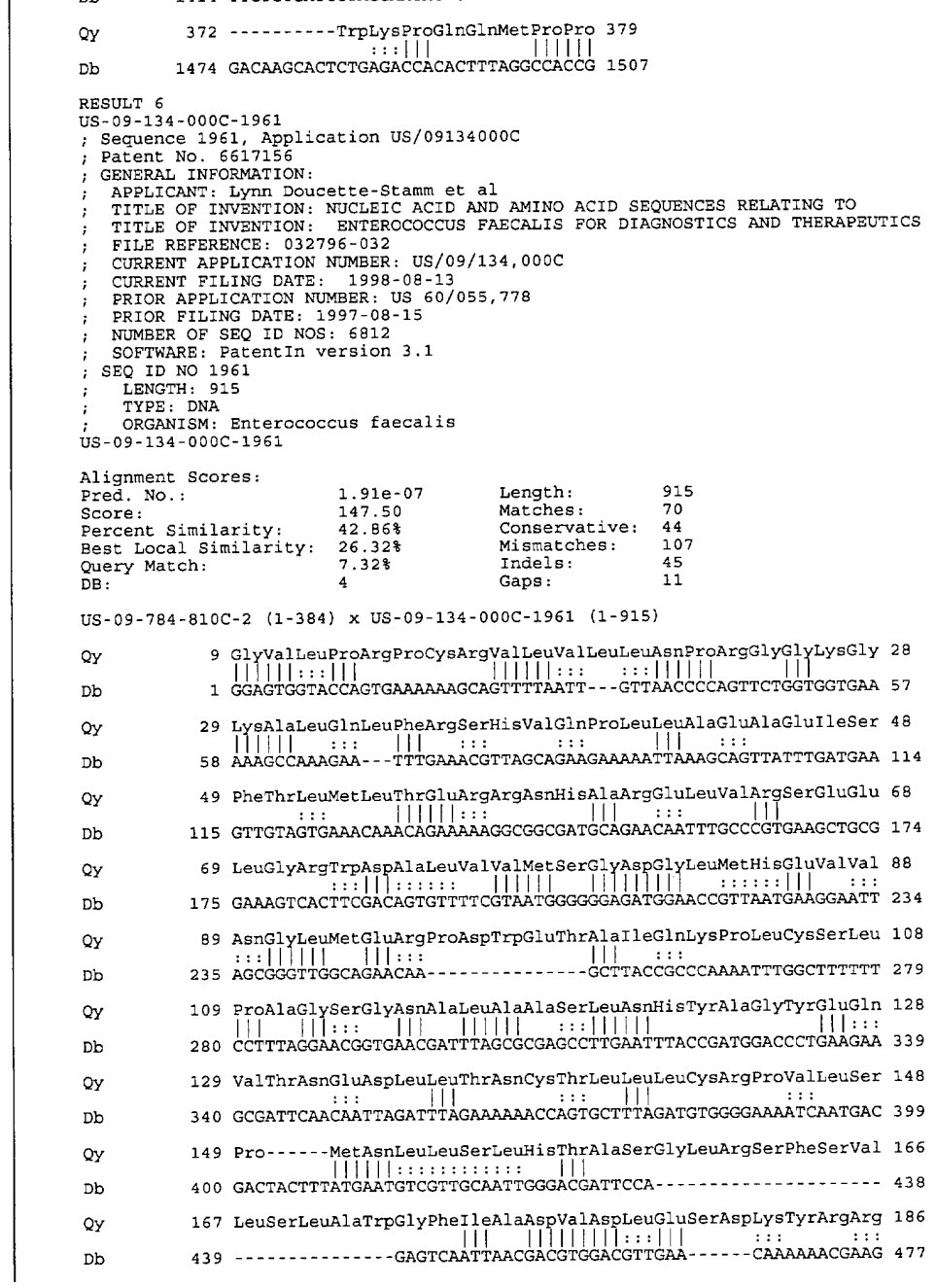
```
Qy        21 LeuAsnProArgGlyGlyLysGlyLysAlaLeuGlnLeuPheArgSerHisValGlnPro 40
Db        61 CTGAACCCGCGCGGCGGCAAGGGCAAGGCCTTGCAGCTCTTCCGGAGTCACGTGCAGCCC 120

Qy        41 LeuLeuAlaGluAlaGluIleSerPheThrLeuMetLeuThrGluArgArgAsnHisAla 60
Db       121 CTTTTGGCTGAGGCTGAAATCTCCTTCACGCTGATGCTCACTGAGCGGCGGAACCACGCG 180

Qy        61 ArgGluLeuValArgSerGluGluLeuGlyArgTrpAspAlaLeuValValMetSerGly 80
Db       181 CGGGAGCTGGTGCGGTCGGAGGAGCTGGGCCGCTGGGACGCTCTGGTGGTCATGTCTGGA 240

Qy        81 AspGlyLeuMetHisGluValValAsnGlyLeuMetGluArgProAspTrpGluThrAla 100
Db       241 GACGGGCTGATGCACGAGGTGGTGAACGGGCTCATGGAGCGGCCTGACTGGGAGACCGCC 300

Qy       101 IleGlnLysProLeuCysSerLeuProAlaGlySerGlyAsnAlaLeuAlaAlaSerLeu 120
Db       301 ATCCAGAAGCCCCTGTGTAGCCTCCCAGCAGGCTCTGGCAACGCGCTGGCAGCTTCCTTG 360

Qy       121 AsnHisTyrAlaGlyTyrGluGlnValThrAsnGluAspLeuLeuThrAsnCysThrLeu 140
Db       361 AACCATTATGCTGGCTATGAGCAGGTCACCAATGAAGACCTCCTGACCAACTGCACGCTA 420

Qy       141 LeuLeuCysArgProValLeuSerProMetAsnLeuLeuSerLeuHisThrAlaSerGly 160
Db       421 TTGCTGTGCCGCCGGCTGCTGTCACCCATGAACCTGCTGTCTCTGCACACGGCTTCGGGG 480

Qy       161 LeuArgSerPheSerValLeuSerLeuAlaTrpGlyPheIleAlaAspValAspLeuGlu 180
Db       481 CTGCGCCTCTTCTCTGTGCTCAGCCTGGCCTGGGGCTTCATTGCTGATGTGGACCTAGAG 540

Qy       181 SerAspLysTyrArgArgLeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgLeu 200
Db       541 AGTGAGAAGTATCGGCGTCTGGGGGAGATGCGCTTCACTCTGGGCACCTTCCTGCGTCTG 600

Qy       201 AlaAlaLeuArgThrTyrArgGlyArgLeuAlaThrLeuProValGlyArgValGlyPhe 220
Db       601 GCAGCCCTGCGCACCTACCGCGGCCGACTGGCCTACCTCCCTGTAGGAAGAGTGGGTTCC 660

Qy       221 LysThrProAlaSerProValValValGlnGlnGlyProValAspAlaHisLeuValPro 240
Db       661 AAGACACCTGCCTCCCCCGTTGTGGTCCAGCAGGGCCCGGTAGATGCACACCTTGTGCCA 720

Qy       241 LeuGluGluGlnValProSerHisTrpGlnValValProAspGluAspPheValLeuVal 260
Db       721 CTGGAGGAGCCAGTGCCCTCTCACTGGACAGTGGTGCCCGACGAGGACTTTGTGCTAGTC 780

Qy       261 LeuAlaLeuLeuHisSerHisLeuAlaSerGluMetPheAlaAlaProMetGlyArgCys 280
Db       781 CTGGCACTGCTGCACTCGCACCTGGGCAGTGAGATGTTTGCTGCACCCATGGGCCGCTGT 840

Qy       281 AlaAlaGlyValMetHisLeuPheTyrValArgAlaGlyValSerArgAlaMetLeuLeu 300
Db       841 GCAGCTGGCGTCATGCATCTGTTCTACGTGCGGGCGGGAGTGTCTCGTGCCATGCTGCTG 900

Qy       301 ArgLeuPheLeuAlaMetGluLysGlyArgHisMetGluTyrGluCysProTyrLeuVal 320
Db       901 CGCCTCTTCCTGGCCATGGAGAAGGGCAGGCATATGGAGTATGAATGCCCCTACTTGGTA 960

Qy       321 TyrValProValValAlaPheArgLeuGluProLysAspGlyLysGlyValPheAlaVal 340
Db       961 TATGTGCCCGTGGTCGCCTTCCGCTTGGAGCCCAAGGATGGGAAAGGTGTGTTTGCAGTG 1020

Qy       341 AspGlyGluLeuMetValSerGluAlaValGlnGlyGlnValHisProAsnTyrPheTrp 360
Db      1021 GATGGGGAATTGATGGTTAGCGAGGCCGTGCAGGGCCAGGTGCACCCAAACTACTTCTGG 1080

Qy       361 MetValSerGlyCysValGluProProProSerTrpLysProGlnGlnMetProProPro 380
Db      1081 ATGGTCAGCGGTTGCGTGGAGCCCCCGCCCAGCTGGAAGCCCCAGCAGATGCCACCGCCA 1140

Qy       381 GluGluProLeu 384
Db      1141 GAAGAGCCCTTA 1152

RESULT 2
US-09-205-258-90
; Sequence 90, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
;  APPLICANT: Young et al.
;  TITLE OF INVENTION: 207 Human Secreted Proteins
;  FILE REFERENCE: PZ007P1
;  CURRENT APPLICATION NUMBER: US/09/205,258
;  CURRENT FILING DATE: 1998-12-04
;  EARLIER APPLICATION NUMBER: PCT/US98/11422
;  EARLIER FILING DATE: 1998-06-04
;  EARLIER APPLICATION NUMBER: 60/048,885
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/049,375
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,881
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,880
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,896
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/049,020
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,876
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,895
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,884
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,894
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,971
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,964
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,882
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,899
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,893
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,900
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,901
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,892
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,915
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/049,019
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,970
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,972
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,916
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/049,373
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,875
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/049,374
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,917
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,949
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,974
```

```
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,883
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,897
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,898
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,962
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,963
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,877
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,878
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/070,923
;  EARLIER FILING DATE: 1997-12-18
;  EARLIER APPLICATION NUMBER: 60/092,921
;  EARLIER FILING DATE: 1998-07-15
;  EARLIER APPLICATION NUMBER: 60/094,657
;  EARLIER FILING DATE: 1998-07-30
;  NUMBER OF SEQ ID NOS: 1227
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (12)
;   OTHER INFORMATION: n equals a,t,g, or c
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (123)
;   OTHER INFORMATION: n equals a,t,g, or c
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1522)
;   OTHER INFORMATION: n equals a,t,g, or c
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1527)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-205-258-90

Alignment Scores:
Pred. No.:              2.89e-214     Length:          1533
Score:                  1927.00       Matches:         371
Percent Similarity:     96.88%        Conservative:    2
Best Local Similarity:  96.36%        Mismatches:      11
Query Match:            95.63%        Indels:          1
DB:                     4             Gaps:            0

US-09-784-810C-2 (1-384) x US-09-205-258-90 (1-1533)

Qy          1 MetAspProAlaGlyGlyProArgGlyValLeuProArgProCysArgValLeuValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||||
Db         73 ATGGATCCAGCGGGCGGCCCCCGGGGCGTGCTCCCGCGGCCCTGCCGGTGNCTGGTGCTG 132

Qy         21 LeuAsnProArgGlyGlyLysGlyLysAlaLeuGlnLeuPheArgSerHisValGlnPro 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        133 CTGAACCCGCGCGGCGGCAAGGGCAAGGCCTTGCAGCTCTTCCGGAGTCACGTGCAGCCC 192

Qy         41 LeuLeuAlaGluAlaGluIleSerPheThrLeuMetLeuThrGluArgArgAsnHisAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 CTTTTGGCTGAGGCTGAAATCTCCTTCACGCTGATGCTCACTGAGCGGCGGAACCACGCG 252

Qy         61 ArgGluLeuValArgSerGluGluLeuGlyArgTrpAspAlaLeuValValMetSerGly 80
              ||||||||||||||||||||||||||||||||||   ||||||||||||||||    |||
Db        253 CGGGARCTGGTGCGGTCGGAGGAGCTGGGCCGCTGGRACGCTCTGGTGGTCATGTYTGGA 312

Qy         81 AspGlyLeuMetHisGluValValAsnGlyLeu-MetGluArgProAspTrpGluThrAl 100
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        313 GACGGGCTGATGCACGAGGTGGTGAACGGGCTTCATGGAGCGGCCTGACTGGGAGACCGC 372

Qy        100 aIleGlnLysProLeuCysSerLeuProAlaGlySerGlyAsnAlaLeuAlaAlaSerLe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        373 CATCCAGAAGCCCCTGTGTAGCCTCCCAGCAGGCTCTGGCAACGCSCTGGCAGCTTCCTT 432

Qy        120 uAsnHisTyrAlaGlyTyrGluGlnValThrAsnGluAspLeuLeuThrAsnCysThrLe 140
              ||||||||||||||||||   |||||||||||||||||||||||||||||||||||||||
Db        433 RAACCATTATGCTGGCTATRAGCAGGTCACCAATGAAGACCTCCTGACCAACTGCACGCT 492

Qy        140 uLeuLeuCysArgProValLeuSerProMetAsnLeuLeuSerLeuHisThrAlaSerGl 160
              ||||||||||||   :::||||||||||||||||||||||||||||||||||||||||||
Db        493 ATTGCTGTGCCGCCGGCTGCTGTCACCCATGAACCTGCTGTCTCTGCACACGGCTTCGGG 552

Qy        160 yLeuArgSerPheSerValLeuSerLeuAlaTrpGlyPheIleAlaAspValAspLeuGl 180
              ||||||   |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        553 GCTGCGCCTCTTCTCTGTGCTCAGCCTGGCCTGGGGCTTCATTGCTGATGTGGACCTAGA 612

Qy        180 uSerAspLysTyrArgArgLeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgLe 200
              ||||:::|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        613 GAGTGAGAAGTATCGGCGTCTGGGGGAGATGCGCTTCACTCTGGGCACCTTCCTGCGTCT 672

Qy        200 uAlaAlaLeuArgThrTyrArgGlyArgLeuAlaThrLeuProValGlyArgValGlyPh 220
              ||||||||||||||||||||||||||||||||||   ||||||||||||||||||||||
Db        673 GGCAGCCCTGCGCACCTACCGCGGCCGACTGGCCTACCTCCCTGTAGGAAGAGTGGGTTC 732

Qy        220 eLysThrProAlaSerProValValValGlnGlnGlyProValAspAlaHisLeuValPr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        733 CAAGACACCTGCCTCCCCCGTTGTGGTCCAGCAGGGCCCGGTAGATGCACACCTTGTGCC 792

Qy        240 oLeuGluGluGlnValProSerHisTrpGlnValValProAspGluAspPheValLeuVa 260
              ||||||||||   |||||||||||||||   |||||||||||||||||||||||||||||
Db        793 ACTGGAGGAGCCAGTGCCCTCTCACTGGACAGTGGTGCCCGACGAGGACTTTGTGCTAGT 852

Qy        260 lLeuAlaLeuLeuHisSerHisLeuAlaSerGluMetPheAlaAlaProMetGlyArgCy 280
              ||||||||||||||||||||||||   |||||||||||||||||||||||||||||||||
Db        853 CCTGGCACTGCTGCACTCGCACCTGGGCAGTGAGATGTTTGCTGCACCCATGGGCCGCTG 912

Qy        280 sAlaAlaGlyValMetHisLeuPheTyrValArgAlaGlyValSerArgAlaMetLeuLe 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        913 TGCAGCTGGCGTCATGCATCTGTTCTACGTGCGGGCGGGAGTGTCTCGTGCCATGCTGCT 972

Qy        300 uArgLeuPheLeuAlaMetGluLysGlyArgHisMetGluTyrGluCysProTyrLeuVa 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        973 GCGCCTCTTCCTGGCCATGGAGAAGGGCAGGCATATGGAGTATGAATGCCCCTACTTGGT 1032

Qy        320 lTyrValProValValAlaPheArgLeuGluProLysAspGlyLysGlyValPheAlaVa 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1033 ATATGTGCCCGTGGTCGCCTTCCGCTTGGAGCCCAAGGATGGGAAAGGTGTGTTTGCAGT 1092

Qy        340 lAspGlyGluLeuMetValSerGluAlaValGlnGlyGlnValHisProAsnTyrPheTr 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1093 GGATGGGGAATTGATGGTTAGCGAGGCCGTGCAGGGCCAGGTGCACCCAAACTACTTCTG 1152

Qy        360 pMetValSerGlyCysValGluProProProSerTrpLysProGlnGlnMetProProPr 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1153 GATGGTCAGCGGTTGCGTGGAGCCCCCGCCCAGCTGGAAGCCCCAGCAGATGCCACCGCC 1212

Qy        380 oGluGluProLeu 384
              |||||||||||||
Db       1213 AGAAGAGCCCTTA 1225

RESULT 3
US-09-970-516-5
; Sequence 5, Application US/09970516
; Patent No. 6610534
; GENERAL INFORMATION:
;  APPLICANT: No. 6610534artis AG
;  TITLE OF INVENTION: Induction of blood vessel formation through administration of
;  TITLE OF INVENTION:  polynucleotides encoding sphingosine kinases
;  FILE REFERENCE: 4-31617
;  CURRENT APPLICATION NUMBER: US/09/970,516
;  CURRENT FILING DATE:  2001-10-04
```

```
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 1149
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1149)
;   OTHER INFORMATION:
US-09-970-516-5

Alignment Scores:
Pred. No.:              6.1e-175        Length:         1149
Score:                  1587.50         Matches:        302
Percent Similarity:     87.99%          Conservative:   35
Best Local Similarity:  78.85%          Mismatches:     45
Query Match:            78.78%          Indels:         1
DB:                     4               Gaps:           1

US-09-784-810C-2 (1-384) x US-09-970-516-5 (1-1149)

Qy          1 MetAspProAlaGlyGlyProArgGlyValLeuProArgProCysArgValLeuValLeu 20
              |||::|||          |||||||||:::|||||||||||||||||||||||||||||||
Db          1 ATGGAACCAGTAGAATGCCCTCGAGGACTGCTCCCACGGCCATGCAGAGTGCTGGTGCTG 60

Qy         21 LeuAsnProArgGlyGlyLysGlyLysAlaLeuGlnLeuPheArgSerHisValGlnPro 40
              |||||||||:::|||||||||||||||||||||||||||:::|||   |||||||||
Db         61 CTGAACCCCCAGGGTGGCAAGGGCAAGGCTCTGCAGCTCTTCCAGAGCCGTGTGCAGCCC 120

Qy         41 LeuLeuAlaGluAlaGluIleSerPheThrLeuMetLeuThrGluArgArgAsnHisAla 60
                 |||   ||||||||||||:::|||   |||:::|||||||||||:::||||||||||
Db        121 TTCCTGGAGGAGGCAGAGATAACCTTTAAACTGATACTCACCGAACGGAAGAACCATGCC 180

Qy         61 ArgGluLeuValArgSerGluGluLeuGlyArgTrpAspAlaLeuValValMetSerGly 80
              ||||||||||||   :::||||||||||||   ||||||||||||   ||||||||||||
Db        181 AGGGAGCTGGTGTGTGCAGAGGAGTTGGGTCACTGGGACGCCCTGGCAGTCATGTCCGGT 240

Qy         81 AspGlyLeuMetHisGluValValAsnGlyLeuMetGluArgProAspTrpGluThrAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GATGGTCTGATGCATGAGGTGGTGAATGGGCTAATGGAACGGCCCGACTGGGAGACTGCC 300

Qy        101 IleGlnLysProLeuCysSerLeuProAlaGlySerGlyAsnAlaLeuAlaAlaSerLeu 120
              |||||||||||||||||||||||||||||   ||||||||||||||||||||||||:::
Db        301 ATCCAGAAACCCCTGTGTAGCCTCCCTGGAGGCTCCGGCAATGCGCTGGCAGCTTCTGTG 360

Qy        121 AsnHisTyrAlaGlyTyrGluGlnValThrAsnGluAspLeuLeuThrAsnCysThrLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||
Db        361 AACCACTATGCTGGGTACGAGCAGGTGACTAATGAAGACCTGCTCATCAACTGCACACTG 420

Qy        141 LeuLeuCysArgProValLeuSerProMetAsnLeuLeuSerLeuHisThrAlaSerGly 160
              ||||||||||||      ||||||||||||||||||||||||||||||||||||||||
Db        421 CTGTTGTGCCGCCGGCGCCTGTCACCCATGAACCTGCTGTCCCTGCACACTGCTTCTGGG 480

Qy        161 LeuArgSerPheSerValLeuSerLeuAlaTrpGlyPheIleAlaAspValAspLeuGlu 180
              ||||||   :::|||||||||||||||:::|||||||||:::|||||||||||||||||
Db        481 CTGCGGCTCTATTCTGTGCTCAGTCTGTCCTGGGGCTTTGTTGCTGACGTGGACCTCGAG 540

Qy        181 SerAspLysTyrArgArgLeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgLeu 200
              |||:::|||||||||||||||||||:::|||||||||:::|||||||||   ||||||
Db        541 AGTGAGAAGTACAGGCGCTTGGGGGAGATTCGTTTCACAGTGGGCACCTTCTTTCGCCTA 600

Qy        201 AlaAlaLeuArgThrTyrArgGlyArgLeuAlaThrLeuProValGlyArgValGlyPhe 220
              |||:::||||||   |||:::|||:::|||||||   ||||||||||   |||
Db        601 GCAAGCCTGCGCATCTACCAAGGCCAACTGGCCTACCTTCCTGTAGGAACTGTGGCCTCT 660

Qy        221 LysThrProAlaSerProValValValGlnGlnGlyProValAspAlaHisLeuValPro 240
              |||   |||||||||      :::|||||:::|||||||||||||   ||||||||||||
Db        661 AAGAGACCCGCCTCT---ACACTGGTGCAGAAGGGCCCCGTCGACACACACCTTGTTCCT 717

Qy        241 LeuGluGluGlnValProSerHisTrpGlnValValProAspGluAspPheValLeuVal 260
              |||||||||   ||||||||||||||   |||||||||:::::|||||||||||||||||
Db        718 CTGGAGGAGCCAGTGCCTTCTCATTGGACTGTGGTACCAGAACAGGACTTTGTCCTGGTG 777

Qy        261 LeuAlaLeuLeuHisSerHisLeuAlaSerGluMetPheAlaAlaProMetGlyArgCys 280
              |||   |||||||||:::|||||||:::|||||:::|||||||||||||||||||||||
Db        778 CTGGTGCTGCTACACACCCACCTGAGCTCCGAGCTGTTTGCAGCACCCATGGGCCGCTGT 837

Qy        281 AlaAlaGlyValMetHisLeuPheTyrValArgAlaGlyValSerArgAlaMetLeuLeu 300
              ||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        838 GAGGCTGGTGTTATGCATCTGTTCTACGTACGTGCGGGGGTGTCAAGGGCTGCGCTGCTG 897

Qy        301 ArgLeuPheLeuAlaMetGluLysGlyArgHisMetGluTyrGluCysProTyrLeuVal 320
              ||||||||||||||||||:::||||||:::||||||||||   :::|||||||||||||
Db        898 CGCCTCTTCCTGGCCATGCAGAAGGGCAAGCATATGGAACTTGACTGTCCATACCTGGTT 957

Qy        321 TyrValProValValAlaPheArgLeuGluProLysAspGlyLysGlyValPheAlaVal 340
              :::||||||||||||||||||||||||||||||:::      :::|||||||||:::|||
Db        958 CATGTGCCCGTGGTTGCTTTCCGCCTGGAGCCCAGGAGCCAGAGGGGCGTGTTTTCTGTG 1017

Qy        341 AspGlyGluLeuMetValSerGluAlaValGlnGlyGlnValHisProAsnTyrPheTrp 360
              ||||||   |||||||||   ||||||||||||||||||||||||||||||||   |||
Db       1018 GATGGAGGGCTGATGGTATGTGAAGCTGTGCAGGGCCAAGTGCACCCAAACTACCTTTGG 1077

Qy        361 MetValSerGlyCysValGluProProProSerTrpLysProGlnGlnMetProProPro 380
              ||||||   |||      :::   |||                :::::   |||||||||
Db       1078 ATGGTCTGTGGCAGCAGAGATGCCCCATCCGGCCGGGACTCCCGGCGGGGGCCACCTCCA 1137

Qy        381 GluGluPro 383
              |||||||||
Db       1138 GAAGAACCA 1146

RESULT 4
US-09-970-516-3
; Sequence 3, Application US/09970516
; Patent No. 6610534
; GENERAL INFORMATION:
;  APPLICANT: No. 6610534artis AG
;  TITLE OF INVENTION: Induction of blood vessel formation through administration of
;  TITLE OF INVENTION:  polynucleotides encoding sphingosine kinases
;  FILE REFERENCE: 4-31617
;  CURRENT APPLICATION NUMBER: US/09/970,516
;  CURRENT FILING DATE:  2001-10-04
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 1857
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1857)
;   OTHER INFORMATION:
US-09-970-516-3

Alignment Scores:
Pred. No.:              1.7e-89         Length:         1857
Score:                  856.50          Matches:        189
Percent Similarity:     51.43%          Conservative:   63
Best Local Similarity:  38.57%          Mismatches:     111
Query Match:            42.51%          Indels:         127
DB:                     4               Gaps:           6

US-09-784-810C-2 (1-384) x US-09-970-516-3 (1-1857)

Qy         10 ValLeuProArgProCysArgValLeuValLeuLeuAsnProArgGlyGlyLysGlyLys 29
              :::|||||||||||   |||:::|||:::|||:::||||||   ||||||:::|||
Db        418 CTGCTACCTCGGCCGCCCCGGTTGCTTCTATTGGTCAATCCCTTTGGGGGTCGGGGCCTG 477

Qy         30 AlaLeuGlnLeuPheArgSerHisValGlnProLeuLeuAlaGluAlaGluIleSerPhe 49
              |||   |||       ::::::|||||   |||:::::::::||||||   :::||||||
Db        478 GCCTGGCAGTGGTGTAAGAACCACGTGCTTCCCATGATCTCTGAAGCTGGGCTGTCCTTC 537

Qy         50 ThrLeuMetLeuThrGluArgArgAsnHisAlaArgGluLeuValArgSerGluGluLeu 69
                 |||:::   |||||||||:::|||||||||||||||||||:::          |||
Db        538 AACCTCATCCAGACAGAACGACAGAACCACGCCCGGGAGCTGGTCCAGGGGCTGAGCCTG 597
```

```
Qy          70 GlyArgTrpAspAlaLeuValValMetSerGlyAspGlyLeuMetHisGluValValAsn 89
Db         598 AGTGAGTGGGATGGCATCGTCACGGTCTCGGGAGACGGGCTGCTCCATGAGGTGCTGAAC 657

Qy          90 GlyLeuMetGluArgProAspTrpGluThrAlaIleGlnLysProLeuCysSerLeuPro 109
Db         658 GGGCTCCTAGATCGCCCTGACTGGGAGGAAGCTGTGAAGATGCCTGTGGGCATCCTCCCC 717

Qy         110 AlaGlySerGlyAsnAlaLeuAlaAlaSerLeuAsnHisTyrAlaGlyTyrGluGlnVal 129
Db         718 TGCGGCTCGGGCAACGCGCTGGCCGGAGCAGTGAACCAGCACGGGGGATTTGAGCCAGCC 777

Qy         130 ThrAsnGluAspLeuLeuThrAsnCysThrLeuLeuLeuCysArgProValLeuSerPro 149
Db         778 CTGGGCCTCGACCTGTTGCTCAACTGCTCACTGTTGCTGTGCCGGGGTGGTGGCCACCCA 837

Qy         150 MetAsnLeuLeuSerLeuHisThrAlaSerGlyLeuArgSerPheSerValLeuSerLeu 169
Db         838 CTGGACCTGCTCTCCGTGACGCTGGCCTCGGGCTCCCGCTGTTTCTCCTTCCTGTCTGTG 897

Qy         170 AlaTrpGlyPheIleAlaAspValAspLeuGluSerAspLysTyrArgArgLeuGlyGlu 189
Db         898 GCCTGGGGCTTCGTGTCAGATGTGGATATCCAGAGCGAGCGCTTCAGGGCCTTGGGCAGT 957

Qy         190 MetArgPheThrLeuGlyThrPheLeuArgLeuAlaAlaLeuArgThrTyrArgGlyArg 209
Db         958 GCCCGCTTCACACTGGGCACGGTGCTGGGCCTCGCCACACTGCACACCTACCGCGGACGC 1017

Qy         210 LeuAlaThrLeuProVal---------------------------------------- 215
Db        1018 CTCTCCTACCTCCCCGCCACTGTGGAACCTGCCTCGCCCACCCCTGCCCATAGCCTGCCT 1077

Qy         215 ------------------------------------------------------------ 215
Db        1078 CGTGCCAAGTCGGAGCTGACCCTAACCCCAGACCCAGCCCCGCCCATGGCCCACTCACCC 1137

Qy         215 ------------------------------------------------------------ 215
Db        1138 CTGCATCGTTCTGTGTCTGACCTGCCTCTTCCCCTGCCCCAGCCTGCCCTGGCCTCTCCT 1197

Qy         215 ------------------------------------------------------------ 215
Db        1198 GGCTCGCCAGAACCCCTGCCCATCCTGTCCCTCAACGGTGGGGGCCCAGAGCTGGCTGGG 1257

Qy         215 ------------------------------------------------------------ 215
Db        1258 GACTGGGGTGGGGCTGGGGATGCTCCGCTGTCCCCGGACCCACTGCTGTCTTCACCTCCT 1317

Qy         216 ------GlyArgValGlyPheLysThrProAlaSer---------ProValValValGln 230
Db        1318 GGCTCTCCCAAGGCAGCTCTACACTCACCCGTCTCCGAAGGGGCCCCCGTAATTCCCCCA 1377

Qy         231 Gln-------------------------------------------------GlyPro 233
Db        1378 TCCTCTGGGCTCCCACTTCCCACCCCTGATGCCCGGGTAGGGGCCTCCACCTGCGGCCCG 1437

Qy         234 ValAspAlaHisLeuValProLeuGluGluGlnValProSerHisTrpGlnValValPro 253
Db        1438 CCCGACCACCTGCTGCCTCCGCTGGGCACCCCGCTGCCCCCAGACTGG---GTGACGCTG 1494

Qy         254 AspGluAspPheValLeuValLeuAlaLeuLeuHisSerHisLeuAlaSerGluMetPhe 273
Db        1495 GAGGGGGACTTTGTGCTCATGTTGGCCATCTCGCCCAGCCACCTAGGCGCTGACCTGGTG 1554

Qy         274 AlaAlaProMetGlyArgCysAlaAlaGlyValMetHisLeuPheTyrValArgAlaGly 293
Db        1555 GCAGCTCCGCATGCGCGCTTCGACGACGGCCTGGTGCACCTGTGCTGGGTGCGTAGCGGC 1614

Qy         294 ValSerArgAlaMetLeuLeuArgLeuPheLeuAlaMetGluLysGlyArgHisMetGlu 313
Db        1615 ATCTCGCGGGCTGCGCTGCTGCGCCTTTTCTTGGCCATGGAGCGTGGTAGCCACTTCAGC 1674

Qy         314 TyrGluCysProTyrLeuValTyrValProValValAlaPheArgLeuGluProLysAsp 333
Db        1675 CTGGGCTGTCCGCAGCTGGGCTACGCCGCGGCCCGTGCCTTCCGCCTAGAGCCGCTCACA 1734

Qy         334 GlyLysGlyValPheAlaValAspGlyGluLeuMetValSerGluAlaValGlnGlyGln 353
Db        1735 CCACGCGGCGTGCTCACAGTGGACGGGGAGCAGGTGGAGTATGGGCCGCTACAGGCACAG 1794

Qy         354 ValHisProAsnTyrPheTrpMetValSerGlyCysValGluProProProSerTrpLys 373
Db        1795 ATGCACCCTGGCATCGGTACACTGCTCACTGGG-----------CCTCCTGGCTGC--- 1839

Qy         374 ProGlnGlnMetProProProGluGluPro 383
Db        1840 --------------CCGGGGCGGGAGCCC 1854

RESULT 5
US-09-620-312D-796
; Sequence 796, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
;  APPLICANT: Tang, Y. Tom
;  APPLICANT:  Liu, Chenghua
;  APPLICANT:  Asundi, Vinod
;  APPLICANT:  Zhang, Jie
;  APPLICANT:  Ren, Feiyan
;  APPLICANT:  Chen, Rui-hong
;  APPLICANT:  Zhao, Qing A.
;  APPLICANT:  Wehrman, Tom
;  APPLICANT:  Xue, Aidong J.
;  APPLICANT:  Yang, Yonghong
;  APPLICANT:  Wang, Jian-Rui
;  APPLICANT:  Zhou, Ping
;  APPLICANT:  Ma, Yunqing
;  APPLICANT:  Wang, Dunrui
;  APPLICANT:  Wang, Zhiwei
;  APPLICANT:  John Tillinghast
;  APPLICANT:  Drmanac, Radoje T.
;  TITLE OF INVENTION: No. 6569662el Nucleic Acids and
;  TITLE OF INVENTION:  Polypeptides
;  FILE REFERENCE: 784CIP2B
;  CURRENT APPLICATION NUMBER: US/09/620,312D
;  CURRENT FILING DATE:  2000-07-19
;  PRIOR APPLICATION NUMBER: 09/552,317
;  PRIOR FILING DATE: 2000-04-25
;  PRIOR APPLICATION NUMBER: 09/488,725
;  PRIOR FILING DATE: 2000-01-21
;  NUMBER OF SEQ ID NOS: 1105
;  SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 796
;   LENGTH: 2462
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (196)..(1464)
US-09-620-312D-796

Alignment Scores:
Pred. No.:              1.24e-12        Length:         2462
Score:                  198.00          Matches:        92
Percent Similarity:     41.02%          Conservative:   77
Best Local Similarity:  22.33%          Mismatches:     160
Query Match:            9.83%           Indels:         83
DB:                     4               Gaps:           18

US-09-784-810C-2 (1-384) x US-09-620-312D-796 (1-2462)

Qy          16 ArgValLeuValLeuLeuAsnProArgGlyGlyLysGlyLysAlaLeuGlnLeuPheArg 35
Db         379 AAGGCCACTGTTTTTCTCAATCCTGCAGCTTGCAAAGGAAAAGCCAGGACTCTATTTGAA 438

Qy          36 SerHisValGlnProLeuLeuAlaGluAlaGluIleSerPheThrLeuMetLeuThrGlu 55
```





RESULT 6
US-09-134-000C-1961
; Sequence 1961, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1961
; LENGTH: 915
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-1961

Alignment Scores:

Pred. No.:	1.91e-07	Length:	915
Score:	147.50	Matches:	70
Percent Similarity:	42.86%	Conservative:	44
Best Local Similarity:	26.32%	Mismatches:	107
Query Match:	7.32%	Indels:	45
DB:	4	Gaps:	11

US-09-784-810C-2 (1-384) x US-09-134-000C-1961 (1-915)

```
Qy        187 LeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgLeuAlaAlaLeuArgThrTyr 206
              ||||||::::::   :::   :::                ||||||      :::||||||
Db        478 TTAGGAAAACTCGCTTATTTTATTTCAGGTGCCAAACATTTAGCGAATGCTCAAACGTAT 537

Qy        207 ArgGlyArgLeu--------------------------------AlaThrLeuProVal 215
                          |||                           :::|||:::   |||
Db        538 CCTTTTCATTTAAGCTTGGATCAAAAAGAACAAACCATTGAAAGTAGTACCGTTTTAGTT 597

Qy        216 GlyArgVal------------GlyPheLysThrProAlaSerProValValValGlnGln 231
              |||                |||||||:::|||                        |||
Db        598 GGCTTAACGAATTCAATCGGTGGGTTTGAAACATTATTACCAGAGGCCCAAGTGGATGAT 657

Qy        232 GlyProValAspAlaHisLeuValProLeuGluGluGlnValProSerHisTrp------ 249
              |||   :::      ||||||||   |||::::::|||      |||   |||
Db        658 GGCAAACTT------CATTTAGTTTATTTAAAAGATCAA------TCATTATGGGATGCA 705

Qy        250 ---GlnValValProAsp 254
                :::   |||||||||
Db        706 GTAAAAGCAGTCCCAGAT 723

RESULT 7
US-09-107-532A-3132
; Sequence 3132, Application US/09107532A
; Patent No. 6583275
;   GENERAL INFORMATION:
;        APPLICANT: Lynn A Doucette-Stamm  and David Bush
;        TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;                            ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
;        NUMBER OF SEQUENCES: 7310
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: GENOME THERAPEUTICS CORPORATION
;             STREET: 100 Beaver Street
;             CITY: Waltham
;             STATE: Massachusetts
;             COUNTRY: USA
;             ZIP: 02354
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD/ROM ISO9660
;             COMPUTER: PC
;             OPERATING SYSTEM: <Unknown>
;             SOFTWARE: ASCII
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/107,532A
;             FILING DATE: 30-Jun-1998
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/085,598
;             FILING DATE: 14 May 1998
;             APPLICATION NUMBER: 60/051571
;             FILING DATE: July 2, 1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Ariniello, Pamela Deneke
;             REGISTRATION NUMBER: 40,489
;             REFERENCE/DOCKET NUMBER: GTC-012
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (781)893-5007
;             TELEFAX: (781)893-8277
;   INFORMATION FOR SEQ ID NO: 3132:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 978 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: circular
;        MOLECULE TYPE: DNA (genomic)
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        ORIGINAL SOURCE:
;             ORGANISM: Enterococcus faecium
;        FEATURE:
;             NAME/KEY:  misc_feature
;             LOCATION: (B) LOCATION 1...978
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3132:
US-09-107-532A-3132
```

```
Alignment Scores:
Pred. No.:                2.32e-05      Length:          978
Score:                    130.00        Matches:         51
Percent Similarity:       40.52%        Conservative:    43
Best Local Similarity:    21.98%        Mismatches:      92
Query Match:              6.45%         Indels:          46
DB:                       4             Gaps:            10

US-09-784-810C-2 (1-384) x US-09-107-532A-3132 (1-978)

Qy         19 ValLeuLeuAsnProArgGlyGlyLysGlyLysAlaLeuGlnLeuPheArgSerHisVal 38
              :::|||:::||||||      |||  |||          ::::::             :::
Db         31 ATATTGATCAATCCATCGGCAGGCAGCGGAAATGGCTATAAAGTA---GCAGAAAGAATT 87

Qy         39 GlnProLeuLeuAlaGluAlaGluIleSerPheThrLeuMetLeuThrGluArgArgAsn 58
                 |||:::|||           |||   :::||||||      :::|||   :::
Db         88 TTACCGGTATTAAAAAATAAGCATATTGACTATACACTTCATTATAGTGAATACAAAGGA 147

Qy         59 HisAlaArgGluLeuValArgSer---------GluGluLeuGlyArgTrp--------- 72
              |||      |||:::      :::         |||  |||      |||
Db        148 CACGATGCTGAGATTGCTGAAACTTTGGCAAAAGAAACATTGATTCCTTGGATAGAAGAA 207

Qy         73 ----------------------AspAlaLeuValValMetSerGlyAspGlyLeuMet 84
                                     |||:::::::::  |||||||||   :::
Db        208 GAACAGAAAACAATCGATACTTTCCCCCTTTTGATCATCGTAGGAGGTGACGGCACCTTA 267

Qy         85 HisGluValValAsnGlyLeuMetGluArgProAspTrpGluThrAlaIleGlnLysPro 104
              |||:::|||::::::                    ::::::      ::::::   |||
Db        268 CATCAGGTACTTGATACTTTC--------------TATCAGATGGAAGTAGAATTCCCA 312

Qy        105 LeuCysSerLeuProAlaGlySerGlyAsnAlaLeuAlaAlaSerLeuAsnHisTyrAla 124
              :::      :::||||||||||||||||||      |||                  |||
Db        313 GTTGCTTATATTCCAGCAGGTTCTGGAAATGATTTTGCTCGAGGG-----------GCA 360

Qy        125 GlyTyrGluGlnValThrAsnGluAspLeuLeuThrAsnCysThrLeuLeuLeuCysArg 144
              |||      :::      :::   |||                |||:::|||
Db        361 GGCCTTCCAAAAAATCCCAAAAAAGGACTT-----------CAGCTGATTTTAGCAGCT 408

Qy        145 ProValLeuSerProMetAsnLeuLeuSerLeu---HisThrAlaSerGlyLeuArgSer 163
                          ::::::::::::::::                |||      :::
Db        409 CAATCACCAGAAAAAGTCCACATAATGGCTTATGAAGAAAAAATAAGTGAAAAAAAAGGA 468

Qy        164 PheSerValLeuSerLeuAlaTrpGlyPhe---------IleAlaAspValAspLeuGlu 180
              :::|||   :::         |||            |||
Db        469 ATAGCTGTTAATAATTTCGGTATAGGATTAGATGCAGCTATCGTCCATGCGACAAATCAT 528

Qy        181 SerAspLysTyrArgArgLeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgLeu 200
              |||       :::|||||      ::::::   ||||||:::|||      |||
Db        529 TCTTCCACAAAAAAGCGATTGAAC------AAATACAACTTAGGATCATTTTCGTATTTA 582

Qy        201 AlaAlaLeuArgThrTyrArgGlyArgLeuAlaThrLeuProValGlyArgValGlyPhe 220
              ::::::                                  |||      |||
Db        583 TTCTCTATTCTC-----------------------------------CGTGCTTTATTC 606

Qy        221 LysThrProAlaSerProValValValGlnGlnGly 232
                        |||::::::|||      |||
Db        607 ACTCAAAAAGGATTTCCAATTCTGGTAGATGCAGGA 642

RESULT 8
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
;  APPLICANT: FLEISCHMAN, Robert D.
;  APPLICANT:  WHITE, Owen R.
;  APPLICANT:  FRASER, Claire M.
;  APPLICANT:  VENTER, John C.
;  TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
;  TITLE OF INVENTION:  TUBERCULOSIS
;  FILE REFERENCE: 24366-20007.00
;  CURRENT APPLICATION NUMBER: US/09/103,840A
;  CURRENT FILING DATE:  1998-06-24
;  NUMBER OF SEQ ID NOS: 2
```

```
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 4403765
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
;   FEATURE:
;   OTHER INFORMATION: CDC 1551
;   OTHER INFORMATION: "n" bases at various positions throughout the sequence
;   OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Alignment Scores:
Pred. No.:              35.2          Length:        4403765
Score:                  127.50        Matches:       41
Percent Similarity:     41.50%        Conservative:  20
Best Local Similarity:  27.89%        Mismatches:    65
Query Match:            6.33%         Indels:        21
DB:                     3             Gaps:          2

US-09-784-810C-2 (1-384) x US-09-103-840A-2 (1-4403765)

Qy          7 ProArgGlyValLeuProArgProCysArgValLeuValLeuLeuAsnProArgGlyGly 26
              |||      ::::::   ||||||      :::   ||||||||||||   |||   |||
Db    3589222 CCGGCCCGCATCGTCACACGGCCTARGCCCATTGCCGTCCTCCTCAACGGCCGACCCGGC 3589281

Qy         27 LysGlyLysAlaLeuGlnLeuPheArgSerHisValGlnProLeuLeu------------ 42
                :::                  |||      ::::::   :::|||
Db    3589282 CCGCATCGTCACACGGCCTAAGCTCGTTGCGTCATGCGTGCAGTGCTGATCGTCAACCCC 3589341

Qy         43 ------------------------------------------------AlaGluAlaGlu 46
                                                              |||:::
Db    3589342 ACTGCGACCGCCACCACACCAGCCGGCCGCGACCTGCTGGCGCACGCCCTCGAAAGCCGC 3589401

Qy         47 IleSerPheThrLeuMetLeuThrGluArgArgAsnHisAlaArgGluLeuValArgSer 66
              :::      |||:::      |||      |||   |||      ||||||   ::::::
Db    3589402 CTTCAGCTCACGGTTGAGCACACCAACCACCGCGGTCACGGGACCGAACTCGGACAGGCG 3589461

Qy         67 GluGluLeuGlyArgTrpAspAlaLeuValValMetSerGlyAspGlyLeuMetHisGlu 86
                        |||   :::||||||      ||||||||   :::
Db    3589462 GCGGTAGCCGACGGGGTGGACCTGGTCGTGGTGCATGGCGGCGATGGCACGGTAAGCGCC 3589521

Qy         87 ValValAsnGlyLeuMetGluArgProAspTrpGluThrAlaIleGlnLysPro---Leu 105
              ||||||||||||::::::   ||||||                        |||   :::
Db    3589522 GTAGTCAACGGCATGCTGGGGCGCCCCGGCACGACGCCGGTCCGACCGGTGCCAGCCGTT 3589581

Qy        106 CysSerLeuProAlaGlySerGlyAsnAlaLeuAlaAlaSerLeuAsnHisTyrAlaGly 125
                ::|||   ||||||   |||   ||||||   :::|||          |||
Db    3589582 GCGGTTGTGCCCGGCGGCTCGGCCAACGTACTAGCTCGCGCGCTAGGGATTTCCGCGGAC 3589641

Qy        126 TyrGluGlnValThrAsnGlu 132
                      ||||||:::
Db    3589642 CCGATCGCTGCCACCAACCAA 3589662

RESULT 9
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
;  APPLICANT: FLEISCHMAN, Robert D.
;  APPLICANT:  WHITE, Owen R.
;  APPLICANT:  FRASER, Claire M.
;  APPLICANT:  VENTER, John C.
;  TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
;  TITLE OF INVENTION:  TUBERCULOSIS
;  FILE REFERENCE: 24366-20007.00
;  CURRENT APPLICATION NUMBER: US/09/103,840A
;  CURRENT FILING DATE:  1998-06-24
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 4411529
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
;   OTHER INFORMATION: H37Rv
US-09-103-840A-1

Alignment Scores:
Pred. No.:              46.2          Length:        4411529
Score:                  126.50        Matches:       43
Percent Similarity:     43.54%        Conservative:  21
Best Local Similarity:  29.25%        Mismatches:    62
Query Match:            6.28%         Indels:        21
DB:                     3             Gaps:          4

US-09-784-810C-2 (1-384) x US-09-103-840A-1 (1-4411529)

Qy          7 ProArgGlyValLeuProArgProCysArgValLeuValLeuLeuAsn---------- 22
              |||      ::::::   ||||||      :::   ||||||||||||
Db    3594372 CCGGCCCGCATCGTCACACGGCCTAAGCCCATTGCCGTCCTCCTCAACGGGCCGACCCGG 3594431

Qy         23 ProArgGlyGlyLysGlyLysAlaLeuGlnLeuPheArgSerHisVal---------- 38
              |||          |||   :::      :::   |||:::   :::
Db    3594432 CCCGCATCGTCACACGGCCTAAGCTCGTGCGTCATGCGTGCAGTGCTGATCGTCAACCCC 3594491

Qy         39 --------------------------GlnProLeuLeuAla---------GluAlaGlu 46
                                        :::   |||||||||         |||:::
Db    3594492 ACTGCGACCGCCACCACACCAGCCGGCCGCGACCTGCTGGCGCACGCCCTCGAAAGCCGC 3594551

Qy         47 IleSerPheThrLeuMetLeuThrGluArgArgAsnHisAlaArgGluLeuValArgSer 66
              :::      |||:::      |||      |||   |||      ||||||   ::::::
Db    3594552 CTTCAGCTCACGGTTGAGCACACCAACCACCGCGGTCACGGGACCGAACTCGGACAGGCG 3594611

Qy         67 GluGluLeuGlyArgTrpAspAlaLeuValValMetSerGlyAspGlyLeuMetHisGlu 86
                        |||   :::||||||      ||||||||   :::
Db    3594612 GCGGTAGCCGACGGGGTGGACCTGGTCGTGGTGCATGGCGGCGATGGCACGGTAAGCGCC 3594671

Qy         87 ValValAsnGlyLeuMetGluArgProAspTrpGluThrAlaIleGlnLysPro---Leu 105
              ||||||||||||::::::   ||||||                        |||   :::
Db    3594672 GTAGTCAACGGCATGCTGGGGCGCCCCGGCACGACGCCGGTCCGACCGGTGCCAGCCGTT 3594731

Qy        106 CysSerLeuProAlaGlySerGlyAsnAlaLeuAlaAlaSerLeuAsnHisTyrAlaGly 125
                ::|||   ||||||   |||   ||||||   :::|||          |||
Db    3594732 GCGGTTGTGCCCGGCGGCTCGGCCAACGTACTAGCTCGCGCGCTAGGGATTTCCGCGGAC 3594791

Qy        126 TyrGluGlnValThrAsnGlu 132
                      ||||||:::
Db    3594792 CCGATCGCTGCCACCAACCAA 3594812

RESULT 10
US-09-134-000C-211
; Sequence 211, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
;  APPLICANT: Lynn Doucette-Stamm et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;  TITLE OF INVENTION:  ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 032796-032
;  CURRENT APPLICATION NUMBER: US/09/134,000C
;  CURRENT FILING DATE:  1998-08-13
;  PRIOR APPLICATION NUMBER: US 60/055,778
;  PRIOR FILING DATE: 1997-08-15
;  NUMBER OF SEQ ID NOS: 6812
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 211
;   LENGTH: 894
;   TYPE: DNA
;   ORGANISM: Enterococcus faecalis
US-09-134-000C-211

Alignment Scores:
Pred. No.:              6.7e-05       Length:        894
Score:                  125.50        Matches:       52
Percent Similarity:     41.89%        Conservative:  41
Best Local Similarity:  23.42%        Mismatches:    75
Query Match:            6.23%         Indels:        54
DB:                     4             Gaps:          10
```

```
US-09-784-810C-2 (1-384) x US-09-134-000C-211 (1-894)

Qy          42 LeuAlaGluAlaGluIleSerPheThrLeuMetLeuThrGluArgArgAsnHisAlaArg 61
               |||   :::   |||:::   :::|||   :::   |||:::          |||   :::
Db          19 CTCAAGCAACAAGAACTTAAATATACGGCTCTTTACACTGATTACGCTGGACATGAAAAA 78

Qy          62 GluLeuValArg----------------------------SerGluGluLeu------ 69
               ||||||   :::                           |||||:::|||
Db          79 GAATTGACGAAGGAACTTGCAGAAACAACTTTACTTCCTTGGTCTGAAGACTTAGACGTT 138

Qy          70 GlyArgTrpAspAlaLeuValValMetSerGlyAspGlyLeuMetHisGluValValAsn 89
                  :::     |||||||||:::   ||||||||   :::|||   |||:::|||
Db         139 TCAACTTTTCCAATCCTAGTCGTGCTAGGCGGCGATGGCACACTACATAATGTCATTAAT 198

Qy          90 GlyLeuMetGluArgProAspTrpGluThrAlaIleGlnLysProLeuCysSerLeuPro 109
                  |||:::          :::::::::   |||     ||||||     :::|||
Db         199 TCATTACTT---------CCATATGATTCAACTATT------CCTTTAAGCTATATTCCA 243

Qy         110 AlaGlySerGlyAsnAlaLeuAlaAlaSerLeuAsnHisTyrAlaGlyTyrGluGlnVal 129
               ||||||||||||      |||      :::                   ::::::
Db         244 TGCGGCTCTGGAAATGATTTTGCACGAGGGGTGGGATTATCAAGAAATATTGATAAAGCA 303

Qy         130 ThrAsnGluAspLeuLeuThrAsnCysThrLeuLeuLeuCysArgProValLeuSerPro 149
               ::::::   |||   |||                                    |||
Db         304 TTGCATCAAATCCTGCGCACCAGA----------------------------CGACCA 333

Qy         150 MetAsnLeuLeuSerLeuHisThrAlaSer-----------------GlyLeuArgSer 163
                  :::   ::::::|||                            |||||   :::
Db         334 AAAGAAATTCAAACAATTCATTATGTAAAAGCCAACCAAGAAGAAATCGGCTTAGCCACC 393

Qy         164 PheSerVal---------LeuSerLeuAlaTrpGlyPheIleAlaAspValAspLeuGlu 180
                  :::|||         |||     |||         |||   :::         |||
Db         394 AATAATGTTGGCTTAGGGTTGGATGCGGCA---------ATCGTGGAAAAAACCAACGAA 444

Qy         181 SerAspLysTyrArgArgLeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgLeu 200
               |||     :::   |||       :::|||   |||||:::       :::
Db         445 TCGTCATCAAAAAAAGCCTTAAAT------AAATTTAAGCTTGGCTCGCTTTCCTATATT 498

Qy         201 AlaAlaLeuArgThrTyrArgGlyArgLeuAlaThrLeuProValGlyArgValGlyPhe 220
               ::::::                                :::     |||   |||
Db         499 TCTTCA----------------------------------ATCATTCATGTCTTTTTT 522

Qy         221 LysThrProAlaSerProValValValGlnGlnGlyProVal-AspAlaHisLeuValPr 240
               :::           |||:::::|||:::           :::   ||||||:::
Db         523 AGACAAAAAGGCTTTCCAATTTTAGTTGAAATGAATGGTAAACAATACACATTTAATCGT 582

Qy         240 oLeu 241
                |||
Db         583 GCTT 586

RESULT 11
US-09-107-532A-3500
; Sequence 3500, Application US/09107532A
; Patent No. 6583275
;   GENERAL INFORMATION:
;        APPLICANT: Lynn A Doucette-Stamm  and David Bush
;        TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;                            ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
;        NUMBER OF SEQUENCES: 7310
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: GENOME THERAPEUTICS CORPORATION
;             STREET: 100 Beaver Street
;             CITY: Waltham
;             STATE: Massachusetts
;             COUNTRY: USA
;             ZIP: 02354
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD/ROM ISO9660
;             COMPUTER: PC
;             OPERATING SYSTEM: <Unknown>
;             SOFTWARE: ASCII
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/107,532A
;             FILING DATE: 30-Jun-1998
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/085,598
;             FILING DATE: 14 May 1998
;             APPLICATION NUMBER: 60/051571
;             FILING DATE: July 2, 1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Ariniello, Pamela Deneke
;             REGISTRATION NUMBER: 40,489
;             REFERENCE/DOCKET NUMBER: GTC-012
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (781)893-5007
;             TELEFAX: (781)893-8277
;    INFORMATION FOR SEQ ID NO: 3500:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 942 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: circular
;        MOLECULE TYPE: DNA (genomic)
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        ORIGINAL SOURCE:
;             ORGANISM: Enterococcus faecium
;        FEATURE:
;             NAME/KEY:  misc_feature
;             LOCATION: (B) LOCATION 1...942
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3500:
US-09-107-532A-3500

Alignment Scores:
Pred. No.:                0.000476        Length:          942
Score:                    118.50          Matches:         53
Percent Similarity:       44.22%          Conservative:    58
Best Local Similarity:    21.12%          Mismatches:      89
Query Match:              5.88%           Indels:          51
DB:                       4               Gaps:            10

US-09-784-810C-2 (1-384) x US-09-107-532A-3500 (1-942)

Qy          16 ArgValLeuValLeuLeuAsnProArgGlyGlyLysGlyLysAlaLeuGlnLeuPheArg 35
               ::::||||||:::::::::||||||      |||      ::::|||            :::
Db          64 AAAGTTTTATTAGTGGTAAACCCCAGTTCAGGCGGTGAACAAGCA------------AAG 111

Qy          36 SerHisValGlnProLeuLeuAlaGluAlaGluIleSerPhe---------ThrLeuMet 52
                     |||       :::|||:::   |||       |||             ::::::
Db         112 GAATTTGAGCAATTAGCGATAGCAAAATTGGAATCGGTGTTTGATGAAGTGGTCGTCTTG 171

Qy          53 LeuThrGluArgArgAsnHisAlaArgGluLeuValArgSerGluGluLeuGlyArgTrp 72
                  |||::::::      |||:::      |||                    :::
Db         172 CATACAAAAAAAGCAGGGGATGCAAAAAACTTTACTCGCGAAGCGGCTACGGAAGGGTAT 231

Qy          73 AspAlaLeuValValMetSerGlyAspGlyLeuMetHisGluValValAsnGlyLeuMet 92
                  ::::::   ||||||   |||||||||   ::::::|||   ::::::|||:::
Db         232 CATAGTGTGTTTGTCATGGGCGGAGATGGAACAGTCAACGAAGGAATCAGTGGAATCGCT 291

Qy          93 Glu---------ArgProAspTrpGluThrAlaIleGlnLysProLeuCysSerLeuPro 109
               |||         ||||||::::::                                  |||
Db         292 GAACAAGAACATCGGCCAAATTTCGGA-----------------------TTTTTCCCA 327

Qy         110 AlaGlySerGlyAsnAlaLeuAlaAlaSerLeuAsnHisTyrAlaGlyTyrGluGlnVal 129
                  |||:::   |||   ||||||   :::|||                  |||:::
Db         328 TTGGGTACGGTGAATGACTTGGCTCGAGCATTAGGGATACCGCTAGAACCTGAGGAAGCG 387

Qy         130 ThrAsnGluAspLeuLeuThrAsnCysThrLeuLeuLeuCysArgProValLeuSerPro 149
                  |||         :::   :::                          :::   |||
Db         388 ATCAATCATTTTTCGATTGAATCA-------------------------GTCAAGCCA 420

Qy         150 MetAsnLeuLeuSerLeuHisThrAlaSerGlyLeuArgSerPheSerValLeuSerLeu 169
                  :::::::::      ::::::                    :::   :::      :::
Db         421 TTGGATATTGGAAAAATAAATGAC--------------GACTATTTTATGAATGTCGTC 465
```

```
Qy        170 AlaTrpGlyPheIleAlaAspVal------AspLeuGluSerAspLysTyrArgArgLeu 187
              |||  |||  |||  :::          |||::::::::::::|||         :::
Db        466 GCAATTGGCTCTATCCCTGAATCAATCAATGATGTAGATGCGGAGAAGAAGACGAAATTT 525

Qy        188 GlyGluMetArgPheThrLeuGlyThrPheLeuArgLeuAlaAlaLeuArgThrTyrArg 207
              |||::::::  :::  :::               :::||||||:::  ::::::|||
Db        526 GGAAAACTAGCTTATTTCATGTCAGGAATCAAACAGTTAGCTTCCACACAATCCTACTCG 585

Qy        208 GlyArgLeu--------------------------------AlaThrLeuProValGly 216
                 :::                                   :::||||||  :::|||
Db        586 TTTCACGTAGAAGTTGATGGAAAGAAGGAAGAAATTGAGAGCAGTACCTTGCTGATAGGA 645

Qy        217 ArgVal------------GlyPheLysThrProAlaSerProValValValGlnGlnGly 232
                                |||||:::|||               |||        |||
Db        646 CTAACTAACTCAGTCGGCGGTTTTGAAACATTACTTCCAAATGCAAAAGTGGATGATGGT 705

Qy        233 ProValAspAlaHisLeuValProLeuGluGlu 243
                 :::       |||||||||  |||::::::
Db        706 AAGCTC------CATTTGGTTTATTTAAAAGAT 732
```

RESULT 12
US-08-961-527-332/c
; Sequence 332, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 332:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 900 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-527-332

Alignment Scores:

Pred. No.:	0.00193	Length:	900
Score:	113.00	Matches:	47
Percent Similarity:	49.39%	Conservative:	34
Best Local Similarity:	28.66%	Mismatches:	54
Query Match:	5.61%	Indels:	29
DB:	4	Gaps:	8

US-09-784-810C-2 (1-384) x US-08-961-527-332 (1-900)

```
Qy         16 ArgValLeuValLeuLeuAsnProArgGlyGlyLysGlyLysAlaLeuGlnLeuPheArg 35
              :::   :::|||::::::::|||||         |||         |||||||||
Db        472 AAAGCAATGGTAATTATCAACCCTACTTCTGGTGGCGAGAAGGCTTTG------------ 425

Qy         36 SerHisValGlnProLeuLeuAlaGluAlaGluIleSerPheThrLeuMet--------- 52
                 :::   :::   |||      :::|||:::         |||      :::
Db        424 GATTACAAAGAAAAGCTGGAGAATAAAGCAAAAGAATACTTTGAATATGTTGAAACCAAA 365

Qy         53 LeuThrGluArgArgAsnHisAlaArgGluLeuValArgSerGluGluLeuGlyArgTrp 72
              :::||||||:::              |||                         ::::::
Db        364 ATTACCGAAAAAGCGCTGGATGCAACACATTTTGCTGAAGAAGCTTCTCGTGAGCAGTAT 305

Qy         73 AspAlaLeuValValMetSerGlyAspGlyLeuMetHisGluValValAsnGlyLeuMet 92
              ||||||:::||||||         |||||||||   ::::::||||||::::::|||:::
Db        304 GATGCAGTGGTTGTGTTTGGTGGAGATGGAACTGTCAATGAAGTCATTTCAGGTATTGAT 245

Qy         93 GluArgProAspTrpGluThrAlaIleGlnLysProLeuCysSerLeuProAlaGlySer 112
              ||||||   |||:::               |||   |||   |||      :::|||   |||:::
Db        244 GAGAGA---GACTAC---------ATTCCTAAG---TTAGGGATTATCCCAGGCGGTACG 200

Qy        113 GlyAsnAlaLeuAlaAlaSerLeuAsnHisTyrAlaGlyTyrGluGlnValThrAsnGlu 132
              ||||||   :::      |||                               |||:::
Db        199 GGTAACCTCATTACAAAACTTTTGGAA-----------------------ATCAATCAA 164

Qy        133 AspLeu---------LeuThrAsnCysThrLeu---------------LeuLeuCysAr 144
              |||:::         |||||||||   |||                  |||:::
Db        163 GACATCGATGGCGCAATTGACGAACTGGATTTTGATTTAACCAATAAGATTGATATCGGT 104

Qy        144 gProValLeuSerProMetAsnLeuLeuSerLeuHisThrAlaSerGlyLeuArgSerPh 164
                 ::::::   :::   ::::::||||||   :::            ||||||   ||
Db        103 AAAGCAAATGACAACTATTTTGGTTATATCTTTAGTATCGGTTCTCTGCCTGAGGCGATT 44

Qy        164 eSerValLeu 167
              |::::::|||
Db         43 CACAATGTTG 34
```

RESULT 13
US-09-134-000C-408
; Sequence 408, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 408
; LENGTH: 1035
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-408

Alignment Scores:

Pred. No.:	0.00242	Length:	1035
Score:	113.00	Matches:	71
Percent Similarity:	33.14%	Conservative:	45
Best Local Similarity:	20.29%	Mismatches:	132
Query Match:	5.61%	Indels:	102
DB:	4	Gaps:	13

US-09-784-810C-2 (1-384) x US-09-134-000C-408 (1-1035)

```
Qy         19 ValLeuLeuAsnProArgGlyGlyLysGlyLysAlaLeuGlnLeuPheArgSerHisVal 38
              |||:::   ||||||      ||||||               :::|||   :::   ::::::
Db         34 GTGATTTATAATCCAACGTCAGGAAAA------------GAGTTAATCAAAAAGAACTTA 81

Qy         39 GlnProLeuLeuAla--------------------GluAlaGluIleSerPheThrLeu 51
                 :::|||:::                        ||||||            |||
Db         82 GCCGATATTTTATCTATTTTAGAAGAATGTGGTTATGAAGCCAGTGCATTTGCGACC--- 138
```

```
Qy         52 MetLeuThrGluArgArgAsnHisAlaArgGluLeuValArgSerGluGluLeuGlyArg 71
Db        139 ------ACACCAGAAGAAAATTCAGCACGCAATGAAGCACATCGTGCTGCGCGGGCAGGA 192

Qy         72 TrpAspAlaLeuValValMetSerGlyAspGlyLeuMetHisGluValValAsnGly--- 90
Db        193 TTTGATTTACTAGTAGCTGCAGGTGGAGATGGGACCATTAATGAAGTCGTGAATGGGATT 252

Qy         91 ------LeuMetGluArgProAspTrpGluThrAlaIleGlnLysProLeuCysSerLeu 108
Db        253 GCTCCGTTGAAGCGGCGCCCT----------------------AAAATGGCTATTATT 288

Qy        109 ProAlaGlySerGlyAsnAlaLeuAlaAlaSerLeuAsnHisTyrAlaGlyTyrGluGln 128
Db        289 CCTGCTGGAACGACGAATGACTATGCACGGGCCTTGAAG---------------------- 327

Qy        129 ValThrAsnGluAspLeuLeuThrAsnCysThrLeuLeuLeuCysArgProValLeuSer 148
Db        328 -----------------ATTCCTCGTGATAATATCGTTAAGGCAGCAGAAGTGATTAAA 369

Qy        149 ProMetAsnLeuLeuSerLeuHisThrAlaSerGlyLeuArgSerPheSerValLeuSer 168
Db        370 AAAAATCAAACTGTCAAAATGGATATTGGCCAAGCCGGCAAAAATTACTTTATCAATATT 429

Qy        169 LeuAlaTrpGlyPheIleAlaAspValAspLeuGluSerAspLysTyrArgArgLeuGly 188
Db        430 GCGGCGGGTGGTCATTTAACGGAACTGACTTATGAAGTTCCG------------------ 471

Qy        189 GluMetArgPheThrLeuGlyThrPheLeuArgLeuAlaAlaLeuArgThrTyrArgGly 208
Db        472 ----------------------------------TCAGAGTTGAAAAGTATTTTTGGT 495

Qy        209 ArgLeuAlaThrLeuProValGly---------------ArgValGlyPheLysThrPro 223
Db        496 TACTTAGCGTACTTAGCCAAAGGAGCCGAAATGTTGCCGCGAGTG--------------- 540

Qy        224 AlaSerProValVal-----------------------ValGlnGlnGlyProValAsp 235
Db        541 ---AAGCCGATTAAAATGCGCATGACGTATGATGAAGGTGTGTACGAAGGCAATGCATCA 597

Qy        236 AlaHisLeuValProLeuGluGluGlnValProSerHisTrpGlnValValProAspGlu 255
Db        598 ATGTTTTTCCTAGGGCTGACTAACTCGGTGGGTGGTTTTGAGCAAATCGTACCAGAT--- 654

Qy        256 AspPheValLeuValLeuAlaLeuLeuHisSerHisLeuAlaSerGluMetPheAlaAla 275
Db        654 ------------------------------------------------------------ 654

Qy        276 ProMetGlyArgCysAlaAlaGlyValMetHisLeuPheTyrValArgAlaGlyValSer 295
Db        655 ------GCTAAATTAGACGATGGTAAGTTTTCATTAATCATTGTAAAAACAGCCAATATT 708

Qy        296 ArgAlaMetLeuLeuArgLeuPheLeuAlaMetGluLysGlyArgHisMetGluTyrGlu 315
Db        709 TTTGAGATTCTTCATTTAGTTGCGTTAATGTTAAATGGTGGAAAGCATGTTGAAGATCAT 768

Qy        316 CysProTyrLeuValTyrValProValValAlaPheArgLeuGlu------ProLysAsp 333
Db        769 ------CGACTGATCTATACAAAGACCAGCTATTTACATGCAGAAACGTTAGAAAAGAAC 822

Qy        334 GlyLysGlyValPheAlaValAspGlyGlu 343
Db        823 AATAAAATGATGATTAATTTAGATGGTGAA 852

RESULT 14
US-09-221-017B-1064/c
; Sequence 1064, Application US/09221017B
; Patent No. 6444799
;  GENERAL INFORMATION:
;    APPLICANT:  Ross, Bruce C.
;    TITLE OF INVENTION:  P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
;    NUMBER OF SEQUENCES:  1120
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 PAGE MILL ROAD
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/221,017B
;      FILING DATE:  23-DEC-1998
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PP1182
;      FILING DATE:  31-DEC-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PP1546
;      FILING DATE:  30-JAN-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PP2911
;      FILING DATE:  09-APR-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/AU98/01023
;      FILING DATE:  10-DEC-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Monroy, Gladys H
;      REGISTRATION NUMBER:  32,430
;      REFERENCE/DOCKET NUMBER:  27340-20021.00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-813-5600
;      TELEFAX:  650-494-0792
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  1064:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1003 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  UNKNOWN
;    ORIGINAL SOURCE:
;      ORGANISM:  PORYPHYROMONAS GINGIVALIS
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1..1003
US-09-221-017B-1064

Alignment Scores:
Pred. No.:                0.00514        Length:          1003
Score:                    110.00         Matches:         82
Percent Similarity:       35.26%         Conservative:    58
Best Local Similarity:    20.65%         Mismatches:      139
Query Match:              5.46%          Indels:          118
DB:                       4              Gaps:            19

US-09-784-810C-2 (1-384) x US-09-221-017B-1064 (1-1003)

Qy         16 ArgValLeuValLeuLeuAsnProArgGlyGlyLysGlyLysAlaLeuGlnLeuPheArg 35
Db        950 AAGATTCTAGCCATTATCAATNCCATATCGGGCATCGGATCG--------------AAA 906

Qy         36 SerHisValGlnProLeuLeuAlaGlu------AlaGluIleSerPheThrLeuMetLeu 53
Db        905 AGCAACATACCGAGCCTTATAGCCGATGTATTCGCCCATGATCCTCACGAACTCTTTATC 846

Qy         54 Thr------GluArgArgAsnHisAlaArgGluLeuValArgSerGluGluLeuGlyArg 71
Db        845 ACCTATTCGCAACGTGCTGGCCATGCACGTGAATTGGCAGCACAAGCAGTGGAGAAGCAT 786
```

```
Qy         72 TrpAspAlaLeuValValMetSerGlyAspGlyLeuMetHisGluValValAsnGlyLeu 91
              :::|||   ::::::   :::   ||||||||   ::::::|||:::          |||
Db        785 TACGACTGCGTCATTGCAGTAGGAGGCGATGGAACGGTGAACGAGATAGCCCAAAGCCTT 726

Qy         92 MetGluArgProAspTrpGluThrAlaIleGlnLysProLeuCysSerLeuProAlaGly 111
                                                  |||      :::|||   |||
Db        725 --------------------CGCTACACCGATGTAGTGCTGGGTATCGTCCCGAAAGGA 687

Qy        112 SerGlyAsnAlaLeuAlaAlaSerLeuAsn----------------------------- 121
              |||||||||   ||||||   :::|||
Db        686 TCAGGCAACGGGTTGGCACGTGCCCTCAAGCTGCCACTCACCGTCGGGAAAGCTCTCGAA 627

Qy        122 ---HisTyrAlaGlyTyrGluGlnValThrAsnGluAspLeuLeuThrAsnCysThrLeu 140
                 ||||||:::   :::                          :::|||
Db        626 GTGATCAGAGCCGGACATGTTCGCACC-----------------ATCGACTGCTGTGAA 585

Qy        141 LeuLeuCysArgProValLeuSerProMetAsnLeuLeuSerLeuHisThrAlaSerGly 160
                 ||||||          |||
Db        584 GCGGATAGTCGCCCTTTCTTTTGCACCTGCGGATTG---------------------- 549

Qy        161 LeuArgSerPheSerValLeuSerLeuAlaTrpGlyPheIleAlaAspValAspLeuGlu 180
                                            ||||||   |||:::|||
Db        548 --------------------------------GGATTCGATGCCGAGGTT--------- 531

Qy        181 SerAspLysTyrArgArgLeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgLeu 200
              |||   |||:::   ::   |||
Db        530 AGCAAGAAATTCGCCCAAGCGGGTAGTCGA---------------------------- 501

Qy        201 AlaAlaLeuArgThrTyrArgGlyArgLeuAlaThrLeuProValGlyArgValGlyPhe 220
                                                    |||   :::   :::
Db        500 ----------------------------------------GGCCCTATCACTTAT 486

Qy        221 LysThrProAlaSerProValValValGlnGlnGlyProValAspAlaHis--------- 237
                          :::|||      |||   |||   :::
Db        485 GCGCGAACCATGATCGAGAGTTACCTCCAAAACGAACCGAAGGATCCAAACTGACGATAG 426

Qy        238 ---LeuValProLeuGlu-GluGlnValProSerHisTrpGlnValValProAspGluAs 256
                 ||||||    |||      |||   |||      :::||||||
Db        425 ACGGCAAATCCTTTGAGGAGAAAGCTTTCCTCGTCAC------TTGGTGCCA-------- 380

Qy        256 pPheValLeuValLeuAlaLeuLeuHisSerHisLeuAlaSerGluMetPheAlaAlaPr 276
                          :::         :::|||         :::   |||||
Db        379 ----------------------ATGCGCCCCAGTATGGCAATAACGCCTTATATCGCTCC 342

Qy        276 oMetGlyArgCysAlaAlaGlyValMetHisLeuPheTyrValArgAlaGly-------- 293
              |:::                |||   |||   :::      :::|||
Db        341 ATTAGCGGATTTGGAGGATGGTAAAATGGATGTAGTTATTATCCGTCCTTTCAATCCATT 282

Qy        294 -ValSerArgAlaMetLeuLeuArgLeuPheLeu---AlaMetGluLysGlyArgHisMe 312
               :::   :::  |||:::||||||      :::          :::::
Db        281 GGAAGCTCCACAATTGGCTTTACAACTCTTTACCAAGCGTATCAACAGCAACTCCAATCT 222

Qy        312 tGlu---TyrGluCysProTyrLeuValTyrValProValValAlaPheArgLeuGluPr 331
              ::::   |||:::         |||:::
Db        221 GGACACCTATAAGGCCGAAAACCTGATCATT--------------------------GA 189

Qy        331 oLysAspGlyLysGlyValPheAlaValAspGlyGlu-LeuMetValSerGluAlaValG 351
               ::::::   :::||||||      :::||||||::: |||      |||   :::
Db        188 GCGTGAGACAGAGGGCGTAATGCACCTCGATGGCGATCCTGTCATGTTCGGTAAGCGCAT 129

Qy        351 lnGlyGlnVal------------HisProAsnTyrPheTrpMetValSerGlyCysValG 367
                                     |||      |||      ::::::         :::|
Db        128 TGAGATCCGCACCTACGGCCGGTCACTCAAGGTATTTG---CTACTGAAACCTACACTTG 72

Qy        367 luProProProSerTrp---LysProGlnGlnMetProProProGlu 381
              ||   |||   |||:::   ||||||   ::::::|||   ||||||
Db         71 AAAGTCCCACCTCTTTCTAAAAACCAAATAAAATCCCGTAACCGGAG 25

RESULT 15
US-08-956-171E-154/c
; Sequence 154, Application US/08956171E
; Patent No. 6593114
;   GENERAL INFORMATION:
;        APPLICANT: Charles Kunsch
;                   Gil H. Choi
;                   Patrick S. Dillon
;                   Craig A. Rosen
;                   Steven C. Barash
;                   Michael R. Fannon
;        TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
;        NUMBER OF SEQUENCES: 5256
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Human Genome Sciences, Inc.
;             STREET: 9410 Key West Avenue
;             CITY: Rockville
;             STATE: Maryland
;             COUNTRY: USA
;             ZIP: 20850
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
;             COMPUTER: HP Vectra 486/33
;             OPERATING SYSTEM: MSDOS version 6.2
;             SOFTWARE: ASCII Text
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/956,171E
;             FILING DATE: 20-Oct-1997
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/009,861
;             FILING DATE: January 5, 1996
;             APPLICATION NUMBER: 08/781,986
;             FILING DATE: January 3, 1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Mark J. Hyman
;             REGISTRATION NUMBER: 46,789
;             REFERENCE/DOCKET NUMBER: PB248P1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (240) 314-1224
;             TELEFAX: (301) 309-8439
;
;   INFORMATION FOR SEQ ID NO: 154:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 13542 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 154:
US-08-956-171E-154

Alignment Scores:
Pred. No.:                0.584          Length:          13542
Score:                    108.00         Matches:         70
Percent Similarity:       35.52%         Conservative:    60
Best Local Similarity:    19.13%         Mismatches:      126
Query Match:              5.36%          Indels:          110
DB:                       4              Gaps:            18

US-09-784-810C-2 (1-384) x US-08-956-171E-154 (1-13542)

Qy         16 ArgValLeuValLeuLeuAsnProArgGlyGlyLysGlyLysAlaLeuGlnLeuPheArg 35
              |||      ::::::   ||||||      ||||||          :::|||||||:::
Db       5619 CGTGCTAGAATCATTTATAACCCGACATCAGGTAAA-----------GAGCTATTTAAA 5572

Qy         36 SerHisValGlnProLeuLeuAlaGluAlaGluIleSerPheThrLeuMetLeuThrGlu 55
                                        |||:::      |||:::      |||
Db       5571 -------------------------AGAGAATTACCTGATGCCTTAATAAAATTAGAA 5539

Qy         56 ArgArgAsnHisAlaArgGluLeuValArgSerGluGluLeuGly--------------- 70
              :::      :::                :::|||::::::|||
Db       5538 AAAGCGGGATATGAAACGAGTGCATATGCAACCGAGAAAATAGGTGATGCCACACTTGAA 5479

Qy         71 --------------------ArgTrpAspAlaLeuValValMetSerGlyAspGlyLeu 83
                                  :::|||   |||:::          |||||||||
Db       5478 GCAGAAAGAGCTATGCATGAAAATTATGATGTATTAATCGCTGCAGGTGGTGATGGAACA 5419

Qy         84 MetHisGluValValAsnGlyLeuMetGluArgProAspTrpGluThrAlaIleGlnLys 103
```

```
Db       5418 TTAAATGAAGTAGTTAATGGTATCGCAGAAAAGCCTAAT--------------CGTCCT 5374

Qy        104 ProLeuCysSerLeuProAlaGlySerGlyAsnAlaLeuAlaAlaSerLeuAsnHisTyr 123

Db       5373 AAGCTAGGTGTCATTCCTATGGGTACTGTTAATGACTTTGGACGTGCATTGCAT------ 5320

Qy        124 AlaGlyTyrGluGlnValThrAsnGluAspLeuLeuThrAsnCysThrLeuLeuLeuCys 143

Db       5319 --------------ATACCTAATGAC------------------------------- 5308

Qy        144 ArgProValLeuSerProMetAsn---LeuLeuSerLeuHisThrAlaSerGlyLeuArg 162

Db       5307 ------ATCATGGGGGCACTTGATGTCATCATTGAAGGTCATTCTACTAAA--------- 5263

Qy        163 SerPheSerValLeuSerLeuAlaTrpGlyPheIleAlaAspValAspLeuGluSerAsp 182

Db       5262 ----------------------------------GTAGATATTGGTAAAATGAATAAT 5239

Qy        183 LysTyrArgArgLeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgLeuAlaAla 202

Db       5238 CGATAC----------------------------------TTTATTAATTTAGCTGCA 5215

Qy        203 LeuArgThrTyrArgGlyArgLeuAlaThrLeuProValGlyArgValGlyPheLysThr 222

Db       5214 ------------GGCGGACAATTGACG--------------CAAGTCTCTTATGAAACA 5182

Qy        223 ProAlaSerProValValValGlnGlnGlyProValAspAlaHisLeuValProLeuGlu 242

Db       5181 CCG---AGTAAATTGAAATCTATTGTTGGTCCATTT---GCTTATTACATCAAAGGTTTC 5128

Qy        243 GluGlnValProSer------------------------------HisTrpGlnValVal 252

Db       5127 GAAATGTTACCTCAAATGAAAGCTGTAGATTTAAGAATTGAATATGATGGTAATGTTTTC 5068

Qy        253 ProAspGluAspPheValLeuValLeuAlaLeuLeuHisSerHisLeuAlaSerGluMet 272

Db       5067 CAAGGAGAAGCATTATTATTCTTTTTAGGTTTAACAAATTCAATGGCAGGATTTGAAAAA 5008

Qy        273 PheAlaAlaProMetGlyArgCysAlaAlaGlyValMetHisLeuPheTyrValArgAla 292

Db       5007 TTA---GTGCCGGACGCTAAGTTAGATGACGGCTATTTTACGTTAATTATAGTTGAAAAA 4951

Qy        293 GlyValSerArgAlaMetLeuLeuArgLeuPheLeuAlaMetGluLysGlyArgHisMet 312

Db       4950 TCA---AACCTTGCAGAACTTGGTCATATTATGACTTTAGCTTCAAGAGGAGAACATACT 4894

Qy        313 GluTyrGluCysProTyrLeuValTyrValProValValAlaPheArgLeuGluProLys 332

Db       4893 AAGCAT------CCTAAAGTTATTTATGAAAAAGCAAAGGCAATTAATATTTCATCA--- 4843

Qy        333 AspGlyLysGlyValPheAlaValAspGlyGluLeuMetValSerGluAlaValGlnGly 352

Db       4842 -----------------TTCACAGACTTACAACTAAATGTAGATGGAGAATATGGTGGT 4801

Qy        353 GlnValHisProAsnTyr 358

Db       4800 AAATTACCAGCGAATTTC 4783
```

Search completed: August 20, 2004, 01:37:43
Job time : 2820 secs

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 20, 2004, 00:51:17 ; Search time 586 Seconds
(without alignments)
3218.872 Million cell updates/sec

Title: US-09-784-810C-2
Perfect score: 2015
Sequence: 1 MDPAGGPRGVLPRPCRVLVL.....CVEPPPSWKPQQMPPPEEPL 384

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3228839 seqs, 2456066551 residues

Total number of hits satisfying chosen parameters: 6457678

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09784810/runat_13082004_091730_20904/app_query.fasta_1.583
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09784810_@CGN_1_1_480_@runat_13082004_091730_20904
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2015	100.0	1600	9	US-09-784-810A-1	Sequence 1, Appli
	2	1962	97.4	1152	16	US-10-348-052-22	Sequence 22, Appl
	3	1962	97.4	1152	17	US-10-622-011-22	Sequence 22, Appl
	4	1962	97.4	1155	9	US-09-970-516-1	Sequence 1, Appli
	5	1962	97.4	1155	17	US-10-619-344-1	Sequence 1, Appli
	6	1962	97.4	1799	15	US-10-354-358-25	Sequence 25, Appl
	7	1959	97.2	1205	17	US-10-642-289-1	Sequence 1, Appli
c	8	1944	96.5	1562	16	US-10-264-237-1180	Sequence 1180, Ap
	9	1927	95.6	1533	10	US-09-933-767-90	Sequence 90, Appl
	10	1927	95.6	1533	13	US-10-004-860-90	Sequence 90, Appl
	11	1927	95.6	1533	15	US-10-023-282-90	Sequence 90, Appl
	12	1594.5	79.1	1759	9	US-09-784-810A-3	Sequence 3, Appli
	13	1587.5	78.8	1149	9	US-09-970-516-5	Sequence 5, Appli
	14	1587.5	78.8	1149	17	US-10-619-344-5	Sequence 5, Appli
	15	875	43.4	2698	9	US-09-817-676A-11	Sequence 11, Appl
	16	856.5	42.5	1857	9	US-09-970-516-3	Sequence 3, Appli
	17	856.5	42.5	1857	17	US-10-619-344-3	Sequence 3, Appli
	18	856.5	42.5	2380	9	US-09-817-676A-13	Sequence 13, Appl
	19	856.5	42.5	2380	15	US-10-354-358-77	Sequence 77, Appl
	20	856.5	42.5	2380	17	US-10-283-975A-515	Sequence 515, App
	21	550	27.3	2629	16	US-10-348-052-24	Sequence 24, Appl
	22	550	27.3	2629	17	US-10-622-011-24	Sequence 24, Appl
	23	492.5	24.4	2609	16	US-10-348-052-25	Sequence 25, Appl
	24	492.5	24.4	2609	17	US-10-622-011-25	Sequence 25, Appl
	25	481	23.9	480	9	US-09-783-590-9248	Sequence 9248, Ap
	26	444.5	22.1	2084	13	US-10-424-599-47396	Sequence 47396, A
	27	436	21.6	801	13	US-10-296-115-69	Sequence 69, Appl
	28	427	21.2	1869	13	US-10-425-114-34806	Sequence 34806, A
	29	402.5	20.0	1833	17	US-10-437-963-30650	Sequence 30650, A
	30	365	18.1	296	9	US-09-777-564-658	Sequence 658, App
	31	365	18.1	296	15	US-10-015-219-658	Sequence 658, App
	32	363	18.0	1172	17	US-10-283-975A-584	Sequence 584, App
	33	360	17.9	199	9	US-09-796-692-2905	Sequence 2905, Ap
	34	360	17.9	199	15	US-10-040-862-2905	Sequence 2905, Ap
	35	360	17.9	199	16	US-10-057-475B-2905	Sequence 2905, Ap
	36	360	17.9	199	16	US-10-154-884B-2905	Sequence 2905, Ap
	37	355.5	17.6	2064	17	US-10-622-011-32	Sequence 32, Appl
	38	344.5	17.1	1916	17	US-10-437-963-58701	Sequence 58701, A
	39	337	16.7	1875	17	US-10-622-011-30	Sequence 30, Appl
c	40	305.5	15.2	832	15	US-10-029-386-20952	Sequence 20952, A
	41	301.5	15.0	1521	13	US-10-168-582-23	Sequence 23, Appl
	42	300	14.9	1394	16	US-10-264-049-204	Sequence 204, App
	43	295	14.6	422	17	US-10-437-963-30651	Sequence 30651, A
	44	286	14.2	1386	17	US-10-437-963-95148	Sequence 95148, A
c	45	275	13.6	507	15	US-10-029-386-7252	Sequence 7252, Ap

ALIGNMENTS

RESULT 1
US-09-784-810A-1
; Sequence 1, Application US/09784810A
; Patent No. US20020082203A1
; GENERAL INFORMATION:
; APPLICANT: RASTELLI, LUCA
; TITLE OF INVENTION: NOVEL SPHINGOSINE KINASES AND NUCLEIC ACIDS ENCODING
; TITLE OF INVENTION: SAME
; FILE REFERENCE: 10716-08
; CURRENT APPLICATION NUMBER: US/09/784,810A
; CURRENT FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/182,360
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/191,261
; PRIOR FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1600
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base

```
;   LOCATION: (1)
;   OTHER INFORMATION: a, t, c, g, other or unknown
US-09-784-810A-1

Alignment Scores:
Pred. No.:              9.52e-247       Length:         1600
Score:                  2015.00         Matches:        384
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     9               Gaps:           0

US-09-784-810C-2 (1-384) x US-09-784-810A-1 (1-1600)

Qy          1 MetAspProAlaGlyGlyProArgGlyValLeuProArgProCysArgValLeuValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        176 ATGGATCCAGCGGGCGGCCCCCGGGGCGTGCTCCCGCGGCCCTGCCGCGTGCTGGTGCTG 235

Qy         21 LeuAsnProArgGlyGlyLysGlyLysAlaLeuGlnLeuPheArgSerHisValGlnPro 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        236 CTGAACCCGCGCGGCGGCAAGGGCAAGGCCTTGCAGCTCTTCCGGAGTCACGTGCAGCCC 295

Qy         41 LeuLeuAlaGluAlaGluIleSerPheThrLeuMetLeuThrGluArgArgAsnHisAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        296 CTTTTGGCTGAGGCTGAAATCTCCTTCACGCTGATGCTCACTGAGCGGCGGAACCACGCG 355

Qy         61 ArgGluLeuValArgSerGluGluLeuGlyArgTrpAspAlaLeuValValMetSerGly 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        356 CGGGAGCTGGTGCGGTCGGAGGAGCTGGGCCGCTGGGACGCTCTGGTGGTCATGTCTGGA 415

Qy         81 AspGlyLeuMetHisGluValValAsnGlyLeuMetGluArgProAspTrpGluThrAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        416 GACGGGCTGATGCACGAGGTGGTGAACGGGCTCATGGAGCGGCCTGACTGGGAGACCGCC 475

Qy        101 IleGlnLysProLeuCysSerLeuProAlaGlySerGlyAsnAlaLeuAlaAlaSerLeu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        476 ATCCAGAAGCCCCTGTGTAGCCTCCCAGCAGGCTCTGGCAACGCGCTGGCAGCTTCCTTG 535

Qy        121 AsnHisTyrAlaGlyTyrGluGlnValThrAsnGluAspLeuLeuThrAsnCysThrLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        536 AACCATTATGCTGGCTATGAGCAGGTCACCAATGAAGACCTCCTGACCAACTGCACGCTA 595

Qy        141 LeuLeuCysArgProValLeuSerProMetAsnLeuLeuSerLeuHisThrAlaSerGly 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        596 TTGCTGTGCCGCCCGGTGCTGTCACCCATGAACCTGCTGTCTCTGCACACGGCTTCGGGG 655

Qy        161 LeuArgSerPheSerValLeuSerLeuAlaTrpGlyPheIleAlaAspValAspLeuGlu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        656 CTGCGCTCGTTCTCTGTGCTCAGCCTGGCCTGGGGCTTCATTGCTGATGTGGACCTAGAG 715

Qy        181 SerAspLysTyrArgArgLeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        716 AGTGATAAGTATCGGCGTCTGGGGGAGATGCGCTTCACTCTGGGCACCTTCCTGCGTCTG 775

Qy        201 AlaAlaLeuArgThrTyrArgGlyArgLeuAlaThrLeuProValGlyArgValGlyPhe 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        776 GCAGCCCTGCGCACCTACCGCGGCCGACTGGCTACCCTCCCTGTAGGAAGAGTGGGTTTC 835

Qy        221 LysThrProAlaSerProValValValGlnGlnGlyProValAspAlaHisLeuValPro 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        836 AAGACACCTGCTTCCCCCGTTGTGGTCCAGCAGGGCCCGGTAGATGCACACCTGGTGCCA 895

Qy        241 LeuGluGluGlnValProSerHisTrpGlnValValProAspGluAspPheValLeuVal 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        896 CTGGAGGAGCAGGTGCCTTCTCACTGGCAGGTGGTGCCCGACGAGGACTTTGTGCTAGTC 955

Qy        261 LeuAlaLeuLeuHisSerHisLeuAlaSerGluMetPheAlaAlaProMetGlyArgCys 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        956 CTGGCACTGCTGCACTCGCACCTGGCCAGTGAGATGTTTGCTGCACCCATGGGCCGCTGT 1015

Qy        281 AlaAlaGlyValMetHisLeuPheTyrValArgAlaGlyValSerArgAlaMetLeuLeu 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1016 GCAGCTGGCGTCATGCATCTGTTCTACGTGCGGGCGGGAGTGTCTCGTGCCATGCTGCTG 1075

Qy        301 ArgLeuPheLeuAlaMetGluLysGlyArgHisMetGluTyrGluCysProTyrLeuVal 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1076 CGCCTCTTCCTGGCCATGGAGAAGGGCAGGCATATGGAGTATGAATGCCCCTACTTGGTA 1135

Qy        321 TyrValProValValAlaPheArgLeuGluProLysAspGlyLysGlyValPheAlaVal 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1136 TATGTGCCCGTGGTCGCCTTCCGCTTGGAGCCCAAGGATGGGAAAGGTGTGTTTGCAGTG 1195

Qy        341 AspGlyGluLeuMetValSerGluAlaValGlnGlyGlnValHisProAsnTyrPheTrp 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1196 GATGGGGAATTGATGGTTAGCGAGGCCGTGCAGGGCCAGGTGCACCCAAACTACTTCTGG 1255

Qy        361 MetValSerGlyCysValGluProProProSerTrpLysProGlnGlnMetProProPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1256 ATGGTCAGCGGTTGCGTGGAGCCCCCGCCCAGCTGGAAGCCCCAGCAGATGCCACCGCCA 1315

Qy        381 GluGluProLeu 384
              ||||||||||||
Db       1316 GAAGAGCCCTTA 1327

RESULT 2
US-10-348-052-22
; Sequence 22, Application US/10348052
; Publication No. US20030219782A1
; GENERAL INFORMATION:
;  APPLICANT: Saba, Julie D.
;  APPLICANT:  Fyrst, Henrik
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION
;  TITLE OF INVENTION:  OF SPHINGOLIPID METABOLISM AND/OR SIGNALING
;  FILE REFERENCE: 200116.405
;  CURRENT APPLICATION NUMBER: US/10/348,052
;  CURRENT FILING DATE:  2003-01-17
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
;   LENGTH: 1152
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-348-052-22

Alignment Scores:
Pred. No.:              3.44e-240       Length:         1152
Score:                  1962.00         Matches:        375
Percent Similarity:     98.18%          Conservative:   2
Best Local Similarity:  97.66%          Mismatches:     7
Query Match:            97.37%          Indels:         0
DB:                     16              Gaps:           0

US-09-784-810C-2 (1-384) x US-10-348-052-22 (1-1152)

Qy          1 MetAspProAlaGlyGlyProArgGlyValLeuProArgProCysArgValLeuValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGATCCAGCGGGCGGCCCCCGGGGCGTGCTCCCGCGGCCCTGCCGCGTGCTGGTGCTG 60

Qy         21 LeuAsnProArgGlyGlyLysGlyLysAlaLeuGlnLeuPheArgSerHisValGlnPro 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTGAACCCGCGCGGCGGCAAGGGCAAGGCCTTGCAGCTCTTCCGGAGTCACGTGCAGCCC 120

Qy         41 LeuLeuAlaGluAlaGluIleSerPheThrLeuMetLeuThrGluArgArgAsnHisAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTTTTGGCTGAGGCTGAAATCTCCTTCACGCTGATGCTCACTGAGCGGCGGAACCACGCG 180

Qy         61 ArgGluLeuValArgSerGluGluLeuGlyArgTrpAspAlaLeuValValMetSerGly 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CGGGAGCTGGTGCGGTCGGAGGAGCTGGGCCGCTGGGACGCTCTGGTGGTCATGTCTGGA 240

Qy         81 AspGlyLeuMetHisGluValValAsnGlyLeuMetGluArgProAspTrpGluThrAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GACGGGCTGATGCACGAGGTGGTGAACGGGCTCATGGAGCGGCCTGACTGGGAGACCGCC 300

Qy        101 IleGlnLysProLeuCysSerLeuProAlaGlySerGlyAsnAlaLeuAlaAlaSerLeu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        301 ATCCAGAAGCCCCTGTGTAGCCTCCCAGCAGGCTCTGGCAACGCGCTGGCAGCTTCCTTG 360

Qy        121 AsnHisTyrAlaGlyTyrGluGlnValThrAsnGluAspLeuLeuThrAsnCysThrLeu 140

Db        361 AACCATTATGCTGGCTATGAGCAGGTCACCAATGAAGACCTCCTGACCAACTGCACGCTA 420

Qy        141 LeuLeuCysArgProValLeuSerProMetAsnLeuLeuSerLeuHisThrAlaSerGly 160

Db        421 TTGCTGTGCCGCCGGCTGCTGTCACCCATGAACCTGCTGTCTCTGCACACGGCTTCGGGG 480

Qy        161 LeuArgSerPheSerValLeuSerLeuAlaTrpGlyPheIleAlaAspValAspLeuGlu 180

Db        481 CTGCGCCTCTTCTCTGTGCTCAGCCTGGCCTGGGGCTTCATTGCTGATGTGGACCTAGAG 540

Qy        181 SerAspLysTyrArgArgLeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgLeu 200

Db        541 AGTGAGAAGTATCGGCGTCTGGGGGAGATGCGCTTCACTCTGGGCACCTTCCTGCGTCTG 600

Qy        201 AlaAlaLeuArgThrTyrArgGlyArgLeuAlaThrLeuProValGlyArgValGlyPhe 220

Db        601 GCAGCCCTGCGCACCTACCGCGGCCGACTGGCCTACCTCCCTGTAGGAAGAGTGGGTTCC 660

Qy        221 LysThrProAlaSerProValValValGlnGlnGlyProValAspAlaHisLeuValPro 240

Db        661 AAGACACCTGCCTCCCCCGTTGTGGTCCAGCAGGGCCCGGTAGATGCACACCTTGTGCCA 720

Qy        241 LeuGluGluGlnValProSerHisTrpGlnValValProAspGluAspPheValLeuVal 260

Db        721 CTGGAGGAGCCAGTGCCCTCTCACTGGACAGTGGTGCCCGACGAGGACTTTGTGCTAGTC 780

Qy        261 LeuAlaLeuLeuHisSerHisLeuAlaSerGluMetPheAlaAlaProMetGlyArgCys 280

Db        781 CTGGCACTGCTGCACTCGCACCTGGGCAGTGAGATGTTTGCTGCACCCATGGGCCGCTGT 840

Qy        281 AlaAlaGlyValMetHisLeuPheTyrValArgAlaGlyValSerArgAlaMetLeuLeu 300

Db        841 GCAGCTGGCGTCATGCATCTGTTCTACGTGCGGGCGGGAGTGTCTCGTGCCATGCTGCTG 900

Qy        301 ArgLeuPheLeuAlaMetGluLysGlyArgHisMetGluTyrGluCysProTyrLeuVal 320

Db        901 CGCCTCTTCCTGGCCATGGAGAAGGGCAGGCATATGGAGTATGAATGCCCCTACTTGGTA 960

Qy        321 TyrValProValValAlaPheArgLeuGluProLysAspGlyLysGlyValPheAlaVal 340

Db        961 TATGTGCCCGTGGTCGCCTTCCGCTTGGAGCCCAAGGATGGGAAAGGTGTGTTTGCAGTG 1020

Qy        341 AspGlyGluLeuMetValSerGluAlaValGlnGlyGlnValHisProAsnTyrPheTrp 360

Db       1021 GATGGGGAATTGATGGTTAGCGAGGCCGTGCAGGGCCAGGTGCACCCAAACTACTTCTGG 1080

Qy        361 MetValSerGlyCysValGluProProProSerTrpLysProGlnGlnMetProProPro 380

Db       1081 ATGGTCAGTGGTTGCGTGGAGCCCCCGCCCAGCTGGAAGCCCCAGCAGATGCCACCGCCA 1140

Qy        381 GluGluProLeu 384

Db       1141 GAAGAGCCCTTA 1152

RESULT 3
US-10-622-011-22
; Sequence 22, Application US/10622011
; Publication No. US20040126834A1
; GENERAL INFORMATION:
;  APPLICANT: Saba, Julie D.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION
;  TITLE OF INVENTION:  OF SPHINGOLIPID METABOLISM AND/OR SIGNALING
;  FILE REFERENCE: 200116.405C1
;  CURRENT APPLICATION NUMBER: US/10/622,011
;  CURRENT FILING DATE:  2003-07-16
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
;   LENGTH: 1152
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-622-011-22

Alignment Scores:
Pred. No.:                3.44e-240       Length:          1152
Score:                    1962.00         Matches:         375
Percent Similarity:       98.18%          Conservative:    2
Best Local Similarity:    97.66%          Mismatches:      7
Query Match:              97.37%          Indels:          0
DB:                       17              Gaps:            0

US-09-784-810C-2 (1-384) x US-10-622-011-22 (1-1152)

Qy          1 MetAspProAlaGlyGlyProArgGlyValLeuProArgProCysArgValLeuValLeu 20

Db          1 ATGGATCCAGCGGGCGGCCCCCGGGGCGTGCTCCCGCGGCCCTGCCGCGTGCTGGTGCTG 60

Qy         21 LeuAsnProArgGlyGlyLysGlyLysAlaLeuGlnLeuPheArgSerHisValGlnPro 40

Db         61 CTGAACCCGCGCGGCGGCAAGGGCAAGGCCTTGCAGCTCTTCCGGAGTCACGTGCAGCCC 120

Qy         41 LeuLeuAlaGluAlaGluIleSerPheThrLeuMetLeuThrGluArgArgAsnHisAla 60

Db        121 CTTTTGGCTGAGGCTGAAATCTCCTTCACGCTGATGCTCACTGAGCGGCGGAACCACGCG 180

Qy         61 ArgGluLeuValArgSerGluGluLeuGlyArgTrpAspAlaLeuValValMetSerGly 80

Db        181 CGGGAGCTGGTGCGGTCGGAGGAGCTGGGCCGCTGGGACGCTCTGGTGGTCATGTCTGGA 240

Qy         81 AspGlyLeuMetHisGluValValAsnGlyLeuMetGluArgProAspTrpGluThrAla 100

Db        241 GACGGGCTGATGCACGAGGTGGTGAACGGGCTCATGGAGCGGCCTGACTGGGAGACCGCC 300

Qy        101 IleGlnLysProLeuCysSerLeuProAlaGlySerGlyAsnAlaLeuAlaAlaSerLeu 120

Db        301 ATCCAGAAGCCCCTGTGTAGCCTCCCAGCAGGCTCTGGCAACGCGCTGGCAGCTTCCTTG 360

Qy        121 AsnHisTyrAlaGlyTyrGluGlnValThrAsnGluAspLeuLeuThrAsnCysThrLeu 140

Db        361 AACCATTATGCTGGCTATGAGCAGGTCACCAATGAAGACCTCCTGACCAACTGCACGCTA 420

Qy        141 LeuLeuCysArgProValLeuSerProMetAsnLeuLeuSerLeuHisThrAlaSerGly 160

Db        421 TTGCTGTGCCGCCGGCTGCTGTCACCCATGAACCTGCTGTCTCTGCACACGGCTTCGGGG 480

Qy        161 LeuArgSerPheSerValLeuSerLeuAlaTrpGlyPheIleAlaAspValAspLeuGlu 180

Db        481 CTGCGCCTCTTCTCTGTGCTCAGCCTGGCCTGGGGCTTCATTGCTGATGTGGACCTAGAG 540

Qy        181 SerAspLysTyrArgArgLeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgLeu 200

Db        541 AGTGAGAAGTATCGGCGTCTGGGGGAGATGCGCTTCACTCTGGGCACCTTCCTGCGTCTG 600

Qy        201 AlaAlaLeuArgThrTyrArgGlyArgLeuAlaThrLeuProValGlyArgValGlyPhe 220

Db        601 GCAGCCCTGCGCACCTACCGCGGCCGACTGGCCTACCTCCCTGTAGGAAGAGTGGGTTCC 660

Qy        221 LysThrProAlaSerProValValValGlnGlnGlyProValAspAlaHisLeuValPro 240

Db        661 AAGACACCTGCCTCCCCCGTTGTGGTCCAGCAGGGCCCGGTAGATGCACACCTTGTGCCA 720

Qy        241 LeuGluGluGlnValProSerHisTrpGlnValValProAspGluAspPheValLeuVal 260

Db        721 CTGGAGGAGCCAGTGCCCTCTCACTGGACAGTGGTGCCCGACGAGGACTTTGTGCTAGTC 780

Qy        261 LeuAlaLeuLeuHisSerHisLeuAlaSerGluMetPheAlaAlaProMetGlyArgCys 280

Db        781 CTGGCACTGCTGCACTCGCACCTGGGCAGTGAGATGTTTGCTGCACCCATGGGCCGCTGT 840

Qy        281 AlaAlaGlyValMetHisLeuPheTyrValArgAlaGlyValSerArgAlaMetLeuLeu 300

Db        841 GCAGCTGGCGTCATGCATCTGTTCTACGTGCGGGCGGGAGTGTCTCGTGCCATGCTGCTG 900
```

```
Qy        301 ArgLeuPheLeuAlaMetGluLysGlyArgHisMetGluTyrGluCysProTyrLeuVal 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CGCCTCTTCCTGGCCATGGAGAAGGGCAGGCATATGGAGTATGAATGCCCCTACTTGGTA 960

Qy        321 TyrValProValValAlaPheArgLeuGluProLysAspGlyLysGlyValPheAlaVal 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TATGTGCCCGTGGTCGCCTTCCGCTTGGAGCCCAAGGATGGGAAAGGTGTGTTTGCAGTG 1020

Qy        341 AspGlyGluLeuMetValSerGluAlaValGlnGlyGlnValHisProAsnTyrPheTrp 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GATGGGGAATTGATGGTTAGCGAGGCCGTGCAGGGCCAGGTGCACCCAAACTACTTCTGG 1080

Qy        361 MetValSerGlyCysValGluProProProSerTrpLysProGlnGlnMetProProPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATGGTCAGTGGTTGCGTGGAGCCCCCGCCCAGCTGGAAGCCCCAGCAGATGCCACCGCCA 1140

Qy        381 GluGluProLeu 384
              ||||||||||||
Db       1141 GAAGAGCCCTTA 1152
```

RESULT 4
US-09-970-516-1
; Sequence 1, Application US/09970516
; Patent No. US20020099029A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020099029A1artis AG
; TITLE OF INVENTION: Induction of blood vessel formation through administration of
; TITLE OF INVENTION: polynucleotides encoding sphingosine kinases
; FILE REFERENCE: 4-31617
; CURRENT APPLICATION NUMBER: US/09/970,516
; CURRENT FILING DATE: 2001-10-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1155)
; OTHER INFORMATION:
US-09-970-516-1

Alignment Scores:

Pred. No.:	3.45e-240	Length:	1155
Score:	1962.00	Matches:	375
Percent Similarity:	98.18%	Conservative:	2
Best Local Similarity:	97.66%	Mismatches:	7
Query Match:	97.37%	Indels:	0
DB:	9	Gaps:	0

US-09-784-810C-2 (1-384) x US-09-970-516-1 (1-1155)

```
Qy          1 MetAspProAlaGlyGlyProArgGlyValLeuProArgProCysArgValLeuValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGATCCAGCGGGCGGCCCCCGGGGCGTGCTCCCGCGGCCCTGCCGCGTGCTGGTGCTG 60

Qy         21 LeuAsnProArgGlyGlyLysGlyLysAlaLeuGlnLeuPheArgSerHisValGlnPro 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTGAACCCGCGCGGCGGCAAGGGCAAGGCCTTGCAGCTCTTCCGGAGTCACGTGCAGCCC 120

Qy         41 LeuLeuAlaGluAlaGluIleSerPheThrLeuMetLeuThrGluArgArgAsnHisAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTTTTGGCTGAGGCTGAAATCTCCTTCACGCTGATGCTCACTGAGCGGCGGAACCACGCG 180

Qy         61 ArgGluLeuValArgSerGluGluLeuGlyArgTrpAspAlaLeuValValMetSerGly 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CGGGAGCTGGTGCGGTCGGAGGAGCTGGGCCGCTGGGACGCTCTGGTGGTCATGTCTGGA 240

Qy         81 AspGlyLeuMetHisGluValValAsnGlyLeuMetGluArgProAspTrpGluThrAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GACGGGCTGATGCACGAGGTGGTGAACGGGCTCATGGAGCGGCCTGACTGGGAGACCGCC 300

Qy        101 IleGlnLysProLeuCysSerLeuProAlaGlySerGlyAsnAlaLeuAlaAlaSerLeu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATCCAGAAGCCCCTGTGTAGCCTCCCAGCAGGCTCTGGCAACGCGCTGGCAGCTTCCTTG 360

Qy        121 AsnHisTyrAlaGlyTyrGluGlnValThrAsnGluAspLeuLeuThrAsnCysThrLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCATTATGCTGGCTATGAGCAGGTCACCAATGAAGACCTCCTGACCAACTGCACGCTA 420

Qy        141 LeuLeuCysArgProValLeuSerProMetAsnLeuLeuSerLeuHisThrAlaSerGly 160
              |||||||||||||  :::||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTGCTGTGCCGCCGGCTGCTGTCACCCATGAACCTGCTGTCTCTGCACACGGCTTCGGGG 480

Qy        161 LeuArgSerPheSerValLeuSerLeuAlaTrpGlyPheIleAlaAspValAspLeuGlu 180
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTGCGCCTCTTCTCTGTGCTCAGCCTGGCCTGGGGCTTCATTGCTGATGTGGACCTAGAG 540

Qy        181 SerAspLysTyrArgArgLeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgLeu 200
              |||:::||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGTGAGAAGTATCGGCGTCTGGGGGAGATGCGCTTCACTCTGGGCACCTTCCTGCGTCTG 600

Qy        201 AlaAlaLeuArgThrTyrArgGlyArgLeuAlaThrLeuProValGlyArgValGlyPhe 220
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||
Db        601 GCAGCCCTGCGCACCTACCGCGGCCGACTGGCCTACCTCCCTGTAGGAAGAGTGGGTTCC 660

Qy        221 LysThrProAlaSerProValValValGlnGlnGlyProValAspAlaHisLeuValPro 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAGACACCTGCCTCCCCCGTTGTGGTCCAGCAGGGCCCGGTAGATGCACACCTTGTGCCA 720

Qy        241 LeuGluGluGlnValProSerHisTrpGlnValValProAspGluAspPheValLeuVal 260
              |||||||||  ||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db        721 CTGGAGGAGCCAGTGCCCTCTCACTGGACAGTGGTGCCCGACGAGGACTTTGTGCTAGTC 780

Qy        261 LeuAlaLeuLeuHisSerHisLeuAlaSerGluMetPheAlaAlaProMetGlyArgCys 280
              ||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db        781 CTGGCACTGCTGCACTCGCACCTGGGCAGTGAGATGTTTGCTGCACCCATGGGCCGCTGT 840

Qy        281 AlaAlaGlyValMetHisLeuPheTyrValArgAlaGlyValSerArgAlaMetLeuLeu 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCAGCTGGCGTCATGCATCTGTTCTACGTGCGGGCGGGAGTGTCTCGTGCCATGCTGCTG 900

Qy        301 ArgLeuPheLeuAlaMetGluLysGlyArgHisMetGluTyrGluCysProTyrLeuVal 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CGCCTCTTCCTGGCCATGGAGAAGGGCAGGCATATGGAGTATGAATGCCCCTACTTGGTA 960

Qy        321 TyrValProValValAlaPheArgLeuGluProLysAspGlyLysGlyValPheAlaVal 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TATGTGCCCGTGGTCGCCTTCCGCTTGGAGCCCAAGGATGGGAAAGGTGTGTTTGCAGTG 1020

Qy        341 AspGlyGluLeuMetValSerGluAlaValGlnGlyGlnValHisProAsnTyrPheTrp 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GATGGGGAATTGATGGTTAGCGAGGCCGTGCAGGGCCAGGTGCACCCAAACTACTTCTGG 1080

Qy        361 MetValSerGlyCysValGluProProProSerTrpLysProGlnGlnMetProProPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATGGTCAGCGGTTGCGTGGAGCCCCCGCCCAGCTGGAAGCCCCAGCAGATGCCACCGCCA 1140

Qy        381 GluGluProLeu 384
              ||||||||||||
Db       1141 GAAGAGCCCTTA 1152
```

RESULT 5
US-10-619-344-1
; Sequence 1, Application US/10619344
; Publication No. US20040086487A1
; GENERAL INFORMATION:
; APPLICANT: Novartis AG
; TITLE OF INVENTION: Induction of blood vessel formation through administration of
; TITLE OF INVENTION: polynucleotides encoding sphingosine kinases
; FILE REFERENCE: 4-31617
; CURRENT APPLICATION NUMBER: US/10/619,344
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: US/09/970,516

```
;  PRIOR FILING DATE: 2001-10-04
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1155
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1155)
;   OTHER INFORMATION:
US-10-619-344-1

Alignment Scores:
Pred. No.:                3.45e-240      Length:          1155
Score:                    1962.00        Matches:         375
Percent Similarity:       98.18%         Conservative:    2
Best Local Similarity:    97.66%         Mismatches:      7
Query Match:              97.37%         Indels:          0
DB:                       17             Gaps:            0

US-09-784-810C-2 (1-384) x US-10-619-344-1 (1-1155)

Qy          1 MetAspProAlaGlyGlyProArgGlyValLeuProArgProCysArgValLeuValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGATCCAGCGGGCGGCCCCCGGGGCGTGCTCCCGCGGCCCTGCCGCGTGCTGGTGCTG 60

Qy         21 LeuAsnProArgGlyGlyLysGlyLysAlaLeuGlnLeuPheArgSerHisValGlnPro 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTGAACCCGCGCGGCGGCAAGGGCAAGGCCTTGCAGCTCTTCCGGAGTCACGTGCAGCCC 120

Qy         41 LeuLeuAlaGluAlaGluIleSerPheThrLeuMetLeuThrGluArgArgAsnHisAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTTTTGGCTGAGGCTGAAATCTCCTTCACGCTGATGCTCACTGAGCGGCGGAACCACGCG 180

Qy         61 ArgGluLeuValArgSerGluGluLeuGlyArgTrpAspAlaLeuValValMetSerGly 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CGGGAGCTGGTGCGGTCGGAGGAGCTGGGCCGCTGGGACGCTCTGGTGGTCATGTCTGGA 240

Qy         81 AspGlyLeuMetHisGluValValAsnGlyLeuMetGluArgProAspTrpGluThrAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GACGGGCTGATGCACGAGGTGGTGAACGGGCTCATGGAGCGGCCTGACTGGGAGACCGCC 300

Qy        101 IleGlnLysProLeuCysSerLeuProAlaGlySerGlyAsnAlaLeuAlaAlaSerLeu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATCCAGAAGCCCCTGTGTAGCCTCCCAGCAGGCTCTGGCAACGCGCTGGCAGCTTCCTTG 360

Qy        121 AsnHisTyrAlaGlyTyrGluGlnValThrAsnGluAspLeuLeuThrAsnCysThrLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCATTATGCTGGCTATGAGCAGGTCACCAATGAAGACCTCCTGACCAACTGCACGCTA 420

Qy        141 LeuLeuCysArgProValLeuSerProMetAsnLeuLeuSerLeuHisThrAlaSerGly 160
              |||||||||||   :::||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTGCTGTGCCGCCGGCTGCTGTCACCCATGAACCTGCTGTCTCTGCACACGGCTTCGGGG 480

Qy        161 LeuArgSerPheSerValLeuSerLeuAlaTrpGlyPheIleAlaAspValAspLeuGlu 180
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTGCGCCTCTTCTCTGTGCTCAGCCTGGCCTGGGGCTTCATTGCTGATGTGGACCTAGAG 540

Qy        181 SerAspLysTyrArgArgLeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgLeu 200
              |||:::||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGTGAGAAGTATCGGCGTCTGGGGGAGATGCGCTTCACTCTGGGCACCTTCCTGCGTCTG 600

Qy        201 AlaAlaLeuArgThrTyrArgGlyArgLeuAlaThrLeuProValGlyArgValGlyPhe 220
              ||||||||||||||||||||||||||||||||    ||||||||||||||||||||||
Db        601 GCAGCCCTGCGCACCTACCGCGGCCGACTGGCCTACCTCCCTGTAGGAAGAGTGGGTTCC 660

Qy        221 LysThrProAlaSerProValValValGlnGlnGlyProValAspAlaHisLeuValPro 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAGACACCTGCCTCCCCCGTTGTGGTCCAGCAGGGCCCGGTAGATGCACACCTTGTGCCA 720

Qy        241 LeuGluGluGlnValProSerHisTrpGlnValValProAspGluAspPheValLeuVal 260
              |||||||||   ||||||||||||||   ||||||||||||||||||||||||||||||

Db        721 CTGGAGGAGCCAGTGCCCTCTCACTGGACAGTGGTGCCCGACGAGGACTTTGTGCTAGTC 780

Qy        261 LeuAlaLeuLeuHisSerHisLeuAlaSerGluMetPheAlaAlaProMetGlyArgCys 280
              ||||||||||||||||||||||||    ||||||||||||||||||||||||||||||||
Db        781 CTGGCACTGCTGCACTCGCACCTGGGCAGTGAGATGTTTGCTGCACCCATGGGCCGCTGT 840

Qy        281 AlaAlaGlyValMetHisLeuPheTyrValArgAlaGlyValSerArgAlaMetLeuLeu 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCAGCTGGCGTCATGCATCTGTTCTACGTGCGGGCGGGAGTGTCTCGTGCCATGCTGCTG 900

Qy        301 ArgLeuPheLeuAlaMetGluLysGlyArgHisMetGluTyrGluCysProTyrLeuVal 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CGCCTCTTCCTGGCCATGGAGAAGGGCAGGCATATGGAGTATGAATGCCCCTACTTGGTA 960

Qy        321 TyrValProValValAlaPheArgLeuGluProLysAspGlyLysGlyValPheAlaVal 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TATGTGCCCGTGGTCGCCTTCCGCTTGGAGCCCAAGGATGGGAAAGGTGTGTTTGCAGTG 1020

Qy        341 AspGlyGluLeuMetValSerGluAlaValGlnGlyGlnValHisProAsnTyrPheTrp 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GATGGGGAATTGATGGTTAGCGAGGCCGTGCAGGGCCAGGTGCACCCAAACTACTTCTGG 1080

Qy        361 MetValSerGlyCysValGluProProProSerTrpLysProGlnGlnMetProProPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATGGTCAGCGGTTGCGTGGAGCCCCCGCCCAGCTGGAAGCCCCAGCAGATGCCACCGCCA 1140

Qy        381 GluGluProLeu 384
              ||||||||||||
Db       1141 GAAGAGCCCTTA 1152

RESULT 6
US-10-354-358-25
; Sequence 25, Application US/10354358
; Publication No. US20030157082A1
; GENERAL INFORMATION:
;  APPLICANT: Millennium Pharmaceuticals, Inc
;  APPLICANT:  Hunter, John Joseph
;  APPLICANT:  MacBeth, Kyle J.
;  APPLICANT:  Tsai, Fong-Ying
;  APPLICANT:  Lesoon, Andrea
;  APPLICANT:  Lightcap, Eric S.
;  APPLICANT:  Williamson, Mark
;  APPLICANT:  Rudolph-Owen, Laura A.
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
;  TITLE OF INVENTION:  CANCER USING 140, 1470, 1686, 2089, 2427, 3702, 5891, 6428,
;  TITLE OF INVENTION:  7181, 7660, 25641, 69583, 49863, 8897, 1682, 17667, 9235,
;  TITLE OF INVENTION:  3703, 14171, 10359, 1660, 1450, 18894, 2088, 32427, 2160,
;  TITLE OF INVENTION:  9252, 9389, 1642, 85269, 10297, 1584, 9525, 14124, 4469,
;  TITLE OF INVENTION:  8990, 2100, 9288, 64698, 10480, 20893, 33230, 1586, 9943,
;  TITLE OF INVENTION:  16334, 68862, 9011, 14031, 6178, 21225, 1420, 32236, 2099,
;  TITLE OF INVENTION:  2150, 26583, 2784, 8941, 9811, 27444, 50566 OR 66428 MOLECULES
;  FILE REFERENCE: MPI02-020P1RNOMNIM
;  CURRENT APPLICATION NUMBER: US/10/354,358
;  CURRENT FILING DATE:  2003-01-30
;  PRIOR APPLICATION NUMBER: US 60/353,600
;  PRIOR FILING DATE: 2002-01-31
;  PRIOR APPLICATION NUMBER: US 60/364,517
;  PRIOR FILING DATE: 2002-03-15
;  PRIOR APPLICATION NUMBER: US 60/371,075
;  PRIOR FILING DATE: 2002-04-09
;  PRIOR APPLICATION NUMBER: US 60/371,507
;  PRIOR FILING DATE: 2002-04-10
;  PRIOR APPLICATION NUMBER: US 60/372,984
;  PRIOR FILING DATE: 2002-04-16
;  PRIOR APPLICATION NUMBER: US 60/374,194
;  PRIOR FILING DATE: 2002-04-19
;  PRIOR APPLICATION NUMBER: US 60/382,995
;  PRIOR FILING DATE: 2002-05-24
;  PRIOR APPLICATION NUMBER: US 60/385,023
;  PRIOR FILING DATE: 2002-05-31
;  PRIOR APPLICATION NUMBER: US 60/388,853
;  PRIOR FILING DATE: 2002-06-14
;  PRIOR APPLICATION NUMBER: US 60/389,395
```

```
;  PRIOR FILING DATE: 2002-06-17
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 122
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
;   LENGTH: 1799
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (359)...(1513)
US-10-354-358-25

Alignment Scores:
Pred. No.:              6.78e-240       Length:         1799
Score:                  1962.00         Matches:        375
Percent Similarity:     98.18%          Conservative:   2
Best Local Similarity:  97.66%          Mismatches:     7
Query Match:            97.37%          Indels:         0
DB:                     15              Gaps:           0

US-09-784-810C-2 (1-384) x US-10-354-358-25 (1-1799)

Qy          1 MetAspProAlaGlyGlyProArgGlyValLeuProArgProCysArgValLeuValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 ATGGATCCAGCGGGCGGCCCCCGGGGCGTGCTCCCGCGGCCCTGCCGCGTGCTGGTGCTG 418

Qy         21 LeuAsnProArgGlyGlyLysGlyLysAlaLeuGlnLeuPheArgSerHisValGlnPro 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        419 CTGAACCCGCGCGGCGGCAAGGGCAAGGCCTTGCAGCTCTTCCGGAGTCACGTGCAGCCC 478

Qy         41 LeuLeuAlaGluAlaGluIleSerPheThrLeuMetLeuThrGluArgArgAsnHisAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        479 CTTTTGGCTGAGGCTGAAATCTCCTTCACGCTGATGCTCACTGAGCGGCGGAACCACGCG 538

Qy         61 ArgGluLeuValArgSerGluGluLeuGlyArgTrpAspAlaLeuValValMetSerGly 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        539 CGGGAGCTGGTGCGGTCGGAGGAGCTGGGCCGCTGGGACGCTCTGGTGGTCATGTCTGGA 598

Qy         81 AspGlyLeuMetHisGluValValAsnGlyLeuMetGluArgProAspTrpGluThrAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        599 GACGGGCTGATGCACGAGGTGGTGAACGGGCTCATGGAGCGGCCTGACTGGGAGACCGCC 658

Qy        101 IleGlnLysProLeuCysSerLeuProAlaGlySerGlyAsnAlaLeuAlaAlaSerLeu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        659 ATCCAGAAGCCCCTGTGTAGCCTCCCAGCAGGCTCTGGCAACGCGCTGGCAGCTTCCTTG 718

Qy        121 AsnHisTyrAlaGlyTyrGluGlnValThrAsnGluAspLeuLeuThrAsnCysThrLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 AACCATTATGCTGGCTATGAGCAGGTCACCAATGAAGACCTCCTGACCAACTGCACGCTA 778

Qy        141 LeuLeuCysArgProValLeuSerProMetAsnLeuLeuSerLeuHisThrAlaSerGly 160
              |||||||||||   :::||||||||||||||||||||||||||||||||||||||||||||
Db        779 TTGCTGTGCCGCCGGCTGCTGTCACCCATGAACCTGCTGTCTCTGCACACGGCTTCGGGG 838

Qy        161 LeuArgSerPheSerValLeuSerLeuAlaTrpGlyPheIleAlaAspValAspLeuGlu 180
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        839 CTGCGCCTCTTCTCTGTGCTCAGCCTGGCCTGGGGCTTCATTGCTGATGTGGACCTAGAG 898

Qy        181 SerAspLysTyrArgArgLeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgLeu 200
              |||:::||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        899 AGTGAGAAGTATCGGCGTCTGGGGGAGATGCGCTTCACTCTGGGCACCTTCCTGCGTCTG 958

Qy        201 AlaAlaLeuArgThrTyrArgGlyArgLeuAlaThrLeuProValGlyArgValGlyPhe 220
              ||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        959 GCAGCCCTGCGCACCTACCGCGGCCGACTGGCCTACCTCCCTGTAGGAAGAGTGGGTTCC 1018

Qy        221 LysThrProAlaSerProValValValGlnGlnGlyProValAspAlaHisLeuValPro 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1019 AAGACACCTGCCTCCCCCGTTGTGGTCCAGCAGGGCCCGGTAGATGCACACCTTGTGCCA 1078

Qy        241 LeuGluGluGlnValProSerHisTrpGlnValValProAspGluAspPheValLeuVal 260
              |||||||||   |||||||||||||||   ||||||||||||||||||||||||||||||
Db       1079 CTGGAGGAGCCAGTGCCCTCTCACTGGACAGTGGTGCCCGACGAGGACTTTGTGCTAGTC 1138

Qy        261 LeuAlaLeuLeuHisSerHisLeuAlaSerGluMetPheAlaAlaProMetGlyArgCys 280
              ||||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||
Db       1139 CTGGCACTGCTGCACTCGCACCTGGGCAGTGAGATGTTTGCTGCACCCATGGGCCGCTGT 1198

Qy        281 AlaAlaGlyValMetHisLeuPheTyrValArgAlaGlyValSerArgAlaMetLeuLeu 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1199 GCAGCTGGCGTCATGCATCTGTTCTACGTGCGGGCGGGAGTGTCTCGTGCCATGCTGCTG 1258

Qy        301 ArgLeuPheLeuAlaMetGluLysGlyArgHisMetGluTyrGluCysProTyrLeuVal 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1259 CGCCTCTTCCTGGCCATGGAGAAGGGCAGGCATATGGAGTATGAATGCCCCTACTTGGTA 1318

Qy        321 TyrValProValValAlaPheArgLeuGluProLysAspGlyLysGlyValPheAlaVal 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1319 TAYGTGCCCGTGGTCGCCTTCCGCTTGGAGCCCAAGGATGGGAAAGGTGTGTTTGCAGTG 1378

Qy        341 AspGlyGluLeuMetValSerGluAlaValGlnGlyGlnValHisProAsnTyrPheTrp 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1379 GATGGGGAATTGATGGTTAGCGAGGCCGTGCAGGGCCAGGTGCACCCAAACTACTTCTGG 1438

Qy        361 MetValSerGlyCysValGluProProProSerTrpLysProGlnGlnMetProProPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1439 ATGGTCAGCGGTTGCGTGGAGCCCCCGCCCAGCTGGAAGCCCCAGCAGATGCCACCGCCA 1498

Qy        381 GluGluProLeu 384
              ||||||||||||
Db       1499 GAAGAGCCCTTA 1510

RESULT 7
US-10-642-289-1
; Sequence 1, Application US/10642289
; Publication No. US20040132053A1
; GENERAL INFORMATION:
;  APPLICANT: PITSON, Stuart M
;  APPLICANT:  Brian, WATTENBERG W
;  APPLICANT:  Pu, XIA
;  APPLICANT:  Richard, D'ANDREA J
;  APPLICANT:  Jennifer, BAMBLE R
;  APPLICANT:  Mathew, VADAS A
;  TITLE OF INVENTION: SPHINGOSINE KINASE ENZYME
;  FILE REFERENCE: PITSON=1
;  CURRENT APPLICATION NUMBER: US/10/642,289
;  CURRENT FILING DATE:  2003-08-18
;  PRIOR APPLICATION NUMBER: US/09/959,897
;  PRIOR FILING DATE: 2001-11-13
;  PRIOR APPLICATION NUMBER: PCT/AU00/00457
;  PRIOR FILING DATE: 2000-05-12
;  PRIOR APPLICATION NUMBER: AU PQ 0339
;  PRIOR FILING DATE: 1999-05-13
;  PRIOR APPLICATION NUMBER: AU PQ 1504
;  PRIOR FILING DATE: 1999-07-08
;  NUMBER OF SEQ ID NOS: 56
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1205
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (33)..(1184)
;   OTHER INFORMATION:
US-10-642-289-1

Alignment Scores:
Pred. No.:              8.91e-240       Length:         1205
Score:                  1959.00         Matches:        374
Percent Similarity:     98.18%          Conservative:   3
Best Local Similarity:  97.40%          Mismatches:     7
Query Match:            97.22%          Indels:         0
DB:                     17              Gaps:           0
```

US-09-784-810C-2 (1-384) x US-10-642-289-1 (1-1205)

```
Qy          1 MetAspProAlaGlyGlyProArgGlyValLeuProArgProCysArgValLeuValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 ATGGATCCAGCGGGCGGCCCCCGGGGCGTGCTCCCGCGGCCCTGCCGCGTGCTGGTGCTG 92

Qy         21 LeuAsnProArgGlyGlyLysGlyLysAlaLeuGlnLeuPheArgSerHisValGlnPro 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 CTGAACCCGCGCGGCGGCAAGGGCAAGGCCTTGCAGCTCTTCCGGAGTCACGTGCAGCCC 152

Qy         41 LeuLeuAlaGluAlaGluIleSerPheThrLeuMetLeuThrGluArgArgAsnHisAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 CTTTTGGCTGAGGCTGAAATCTCCTTCACGCTGATGCTCACTGAGCGGCGGAACCACGCG 212

Qy         61 ArgGluLeuValArgSerGluGluLeuGlyArgTrpAspAlaLeuValValMetSerGly 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 CGGGAGCTGGTGCGGTCGGAGGAGCTGGGCCGCTGGGACGCTCTGGTGGTCATGTCTGGA 272

Qy         81 AspGlyLeuMetHisGluValValAsnGlyLeuMetGluArgProAspTrpGluThrAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        273 GACGGGCTGATGCACGAGGTGGTGAACGGGCTCATGGAGCGGCCTGACTGGGAGACCGCC 332

Qy        101 IleGlnLysProLeuCysSerLeuProAlaGlySerGlyAsnAlaLeuAlaAlaSerLeu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        333 ATCCAGAAGCCCCTGTGTAGCCTCCCAGCAGGCTCTGGCAACGCGCTGGCAGCTTCCTTG 392

Qy        121 AsnHisTyrAlaGlyTyrGluGlnValThrAsnGluAspLeuLeuThrAsnCysThrLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 AACCATTATGCTGGCTATGAGCAGGTCACCAATGAAGACCTCCTGACCAACTGCACGCTA 452

Qy        141 LeuLeuCysArgProValLeuSerProMetAsnLeuLeuSerLeuHisThrAlaSerGly 160
              |||||||||||   :::||||||||||||||||||||||||||||||||||||||||||||
Db        453 TTGCTGTGCCGCCGGCTGCTGTCACCCATGAACCTGCTGTCTCTGCACACGGCTTCGGGG 512

Qy        161 LeuArgSerPheSerValLeuSerLeuAlaTrpGlyPheIleAlaAspValAspLeuGlu 180
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        513 CTGCGCCTCTTCTCTGTGCTCAGCCTGGCCTGGGGCTTCATTGCTGATGTGGACCTAGAG 572

Qy        181 SerAspLysTyrArgArgLeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgLeu 200
              |||:::||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        573 AGTGAGAAGTATCGGCGTCTGGGGGAGATGCGCTTCACTCTGGGCACTTTCCTGCGTCTG 632

Qy        201 AlaAlaLeuArgThrTyrArgGlyArgLeuAlaThrLeuProValGlyArgValGlyPhe 220
              ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db        633 GCAGCCTTGCGCACTTACCGCGGCCGACTGGCTTACCTCCCTGTAGGAAGAGTGGGTTCC 692

Qy        221 LysThrProAlaSerProValValValGlnGlnGlyProValAspAlaHisLeuValPro 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGACACCTGCCTCCCCCGTTGTGGTCCAGCAGGGCCCGGTAGATGCACACCTTGTGCCA 752

Qy        241 LeuGluGluGlnValProSerHisTrpGlnValValProAspGluAspPheValLeuVal 260
              |||||||||   ||||||||||||||||   ||||||||||||||||||||||||||||||
Db        753 CTGGAGGAGCCAGTGCCCTCTCACTGGACAGTGGTGCCCGACGAGGACTTTGTGCTAGTC 812

Qy        261 LeuAlaLeuLeuHisSerHisLeuAlaSerGluMetPheAlaAlaProMetGlyArgCys 280
              ||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db        813 CTGGCACTGCTGCACTCGCACCTGGGCAGTGAGATGTTTGCTGCACCCATGGGCCGCTGT 872

Qy        281 AlaAlaGlyValMetHisLeuPheTyrValArgAlaGlyValSerArgAlaMetLeuLeu 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 GCAGCTGGCGTCATGCATCTGTTCTACGTGCGGGCGGGAGTGTCTCGTGCCATGCTGCTG 932

Qy        301 ArgLeuPheLeuAlaMetGluLysGlyArgHisMetGluTyrGluCysProTyrLeuVal 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 CGCCTCTTCCTGGCCATGGAGAAGGGCAGGCATATGGAGTATGAATGCCCCTACTTGGTA 992

Qy        321 TyrValProValValAlaPheArgLeuGluProLysAspGlyLysGlyValPheAlaVal 340
              ||||||||||||||||||||||||||||||||||||||||||||||:::||||||||||||
Db        993 TATGTGCCCGTGGTCGCCTTCCGCTTGGAGCCCAAGGATGGGAAAGGTATGTTTGCAGTG 1052

Qy        341 AspGlyGluLeuMetValSerGluAlaValGlnGlyGlnValHisProAsnTyrPheTrp 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GATGGGGAATTGATGGTTAGCGAGGCCGTGCAGGGCCAGGTGCACCCAAACTACTTCTGG 1112

Qy        361 MetValSerGlyCysValGluProProProSerTrpLysProGlnGlnMetProProPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 ATGGTCAGCGGTTGCGTGGAGCCCCCGCCCAGCTGGAAGCCCCAGCAGATGCCACCGCCA 1172

Qy        381 GluGluProLeu 384
              ||||||||||||
Db       1173 GAAGAGCCCTTA 1184
```

RESULT 8
US-10-264-237-1180/c
; Sequence 1180, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 1180
; LENGTH: 1562
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (7)..(7)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (12)..(12)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-264-237-1180

Alignment Scores:

Pred. No.:	1.09e-237	Length:	1562
Score:	1944.00	Matches:	372
Percent Similarity:	98.16%	Conservative:	2
Best Local Similarity:	97.64%	Mismatches:	7
Query Match:	96.48%	Indels:	0
DB:	16	Gaps:	0

US-09-784-810C-2 (1-384) x US-10-264-237-1180 (1-1562)

```
Qy          4 AlaGlyGlyProArgGlyValLeuProArgProCysArgValLeuValLeuLeuAsnPro 23
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1453 GCGGGCGGCCCCCGGGGCGTGCTCCCGCGGCCCTGCCGCGTGCTGGTGCTGCTGAACCCG 1394

Qy         24 ArgGlyGlyLysGlyLysAlaLeuGlnLeuPheArgSerHisValGlnProLeuLeuAla 43
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1393 CGCGGCGGCAAGGGCAAGGCCTTGCAGCTCTTCCGGAGTCACGTGCAGCCCCTTTTGGCT 1334

Qy         44 GluAlaGluIleSerPheThrLeuMetLeuThrGluArgArgAsnHisAlaArgGluLeu 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1333 GAGGCTGAAATCTCCTTCACGCTGATGCTCACTGAGCGGCGGAACCACGCGCGGGAGCTG 1274

Qy         64 ValArgSerGluGluLeuGlyArgTrpAspAlaLeuValValMetSerGlyAspGlyLeu 83
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1273 GTGCGGTCGGAGGAGCTGGGCCGCTGGGACGCTCTGGTGGTCATGTCTGGAGACGGGCTG 1214

Qy         84 MetHisGluValValAsnGlyLeuMetGluArgProAspTrpGluThrAlaIleGlnLys 103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1213 ATGCACGAGGTGGTGAACGGGCTCATGGAGCGGCCTGACTGGGAGACCGCCATCCAGAAG 1154

Qy        104 ProLeuCysSerLeuProAlaGlySerGlyAsnAlaLeuAlaAlaSerLeuAsnHisTyr 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1153 CCCCTGTGTAGCCTCCCAGCAGGCTCTGGCAACGCGCTGGCAGCTTCCTTGAACCATTAT 1094
```

```
Qy        124 AlaGlyTyrGluGlnValThrAsnGluAspLeuLeuThrAsnCysThrLeuLeuLeuCys 143
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1093 GCTGGCTATGAGCAGGTCACCAATGAAGACCTCCTGACCAACTGCACGCTATTGCTGTGC 1034

Qy        144 ArgProValLeuSerProMetAsnLeuLeuSerLeuHisThrAlaSerGlyLeuArgSer 163
              |||   :::||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1033 CGCCGGCTGCTGTCACCCATGAACCTGCTGTCTCTGCACACGGCTTCGGGGCTGCGCCTC 974

Qy        164 PheSerValLeuSerLeuAlaTrpGlyPheIleAlaAspValAspLeuGluSerAspLys 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||
Db        973 TTCTCTGTGCTCAGCCTGGCCTGGGGCTTCATTGCTGATGTGGACCTAGAGAGTGAGAAG 914

Qy        184 TyrArgArgLeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgLeuAlaAlaLeu 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        913 TATCGGCGTCTGGGGGAGATGCGCTTCACTCTGGGCACCTTCCTGCGTCTGGCAGCCCTG 854

Qy        204 ArgThrTyrArgGlyArgLeuAlaThrLeuProValGlyArgValGlyPheLysThrPro 223
              ||||||||||||||||||||    ||||||||||||||||||    |||||||||
Db        853 CGCACCTACCGCGGCCGACTGGCCTACCTCCCTGTAGGAAGAGTGGGTTCCAAGACACCT 794

Qy        224 AlaSerProValValValGlnGlnGlyProValAspAlaHisLeuValProLeuGluGlu 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        793 GCCTCCCCCGTTGTGGTCCAGCAGGGCCCGGTAGATGCACACCTTGTGCCACTGGAGGAG 734

Qy        244 GlnValProSerHisTrpGlnValValProAspGluAspPheValLeuValLeuAlaLeu 263
              ||||||||||||||    ||||||||||||||||||||||||||||||||||||||||||||
Db        733 CCAGTGCCCTCTCACTGGACAGTGGTGCCCGACGAGGACTTTGTGCTAGTCCTGGCACTG 674

Qy        264 LeuHisSerHisLeuAlaSerGluMetPheAlaAlaProMetGlyArgCysAlaAlaGly 283
              ||||||||||||||    ||||||||||||||||||||||||||||||||||||||||||||
Db        673 CTGCACTCGCACCTGGGCAGTGAGATGTTTGCTGCACCCATGGGCCGCTGTGCAGCTGGC 614

Qy        284 ValMetHisLeuPheTyrValArgAlaGlyValSerArgAlaMetLeuLeuArgLeuPhe 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        613 GTCATGCATCTGTTCTACGTGCGGGCGGGAGTGTCTCGTGCCATGCTGCTGCGCCTCTTC 554

Qy        304 LeuAlaMetGluLysGlyArgHisMetGluTyrGluCysProTyrLeuValTyrValPro 323
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        553 CTGGCCATGGAGAAGGGCAGGCATATGGAGTATGAATGCCCCTACTTGGTATATGTGCCC 494

Qy        324 ValValAlaPheArgLeuGluProLysAspGlyLysGlyValPheAlaValAspGlyGlu 343
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        493 GTGGTCGCCTTCCGCTTGGAGCCCAAGGATGGGAAAGGTGTGTTTGCAGTGGATGGGGAA 434

Qy        344 LeuMetValSerGluAlaValGlnGlyGlnValHisProAsnTyrPheTrpMetValSer 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        433 TTGATGGTTAGCGAGGCCGTGCAGGGCCAGGTGCACCCAAACTACTTCTGGATGGTCAGC 374

Qy        364 GlyCysValGluProProProSerTrpLysProGlnGlnMetProProProGluGluPro 383
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        373 GGTTGCGTGGAGCCCCCGCCCAGCTGGAAGCCCCAGCAGATGCCACCGCCAGAAGAGCCC 314

Qy        384 Leu 384
              |||
Db        313 TTA 311
```

RESULT 9
US-09-933-767-90
; Sequence 90, Application US/09933767
; Publication No. US20030181692A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: PZ007P2
; CURRENT APPLICATION NUMBER: US/09/933,767
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: PCT/US01/05614
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/184,836
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/193,170
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/205,258
; PRIOR FILING DATE: 1998-12-04
; PRIOR APPLICATION NUMBER: PCT/US98/11422
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/048,885
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,375
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,881
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,880
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,896
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,020
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,876
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,895
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,884
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,894
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,971
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,964
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,882
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,899
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,893
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,900
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,901
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,892
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,915
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,019
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,972
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,916
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,373
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,875
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,374
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,917
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,949
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,974
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,883
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,897
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,898
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,962
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,963
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,877
; PRIOR FILING DATE: 1997-06-06

```
;  PRIOR APPLICATION NUMBER: 60/048,878
;  PRIOR FILING DATE: 1997-06-06
;  PRIOR APPLICATION NUMBER: 60/068,054
;  PRIOR FILING DATE: 1997-12-18
;  PRIOR APPLICATION NUMBER: 60/068,064
;  PRIOR FILING DATE: 1997-12-18
;  PRIOR APPLICATION NUMBER: 60/068,053
;  PRIOR FILING DATE: 1997-12-18
;  PRIOR APPLICATION NUMBER: 60/070,923
;  PRIOR FILING DATE: 1997-12-18
;  PRIOR APPLICATION NUMBER: 60/073,160
;  PRIOR FILING DATE: 1998-01-30
;  PRIOR APPLICATION NUMBER: 60/073,159
;  PRIOR FILING DATE: 1998-01-30
;  PRIOR APPLICATION NUMBER: 60/073,165
;  PRIOR FILING DATE: 1998-01-30
;  PRIOR APPLICATION NUMBER: 60/073,164
;  PRIOR FILING DATE: 1998-01-30
;  PRIOR APPLICATION NUMBER: 60/085,925
;  PRIOR FILING DATE: 1998-05-18
;  PRIOR APPLICATION NUMBER: 60/085,921
;  PRIOR FILING DATE: 1998-05-18
;  PRIOR APPLICATION NUMBER: 60/085,923
;  PRIOR FILING DATE: 1998-05-18
;  PRIOR APPLICATION NUMBER: 60/085,922
;  PRIOR FILING DATE: 1998-05-18
;  PRIOR APPLICATION NUMBER: 60/092,921
;  PRIOR FILING DATE: 1998-07-15
;  PRIOR APPLICATION NUMBER: 60/094,657
;  PRIOR FILING DATE: 1998-07-30
;  NUMBER OF SEQ ID NOS: 1245
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (12)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: SITE
;   LOCATION: (123)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: SITE
;   LOCATION: (1522)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: SITE
;   LOCATION: (1527)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-933-767-90

Alignment Scores:
Pred. No.:                1.58e-235      Length:          1533
Score:                    1927.00        Matches:         371
Percent Similarity:       96.88%         Conservative:    2
Best Local Similarity:    96.36%         Mismatches:      11
Query Match:              95.63%         Indels:          1
DB:                       10             Gaps:            0

US-09-784-810C-2 (1-384) x US-09-933-767-90 (1-1533)

Qy          1 MetAspProAlaGlyGlyProArgGlyValLeuProArgProCysArgValLeuValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         73 ATGGATCCAGCGGGCGGCCCCCGGGGCGTGCTCCCGCGGCCCTGCCGGTGNCTGGTGCTG 132

Qy         21 LeuAsnProArgGlyGlyLysGlyLysAlaLeuGlnLeuPheArgSerHisValGlnPro 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        133 CTGAACCCGCGCGGCGGCAAGGGCAAGGCCTTGCAGCTCTTCCGGAGTCACGTGCAGCCC 192

Qy         41 LeuLeuAlaGluAlaGluIleSerPheThrLeuMetLeuThrGluArgArgAsnHisAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 CTTTTGGCTGAGGCTGAAATCTCCTTCACGCTGATGCTCACTGAGCGGCGGAACCACGCG 252

Qy         61 ArgGluLeuValArgSerGluGluLeuGlyArgTrpAspAlaLeuValValMetSerGly 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 CGGGARCTGGTGCGGTCGGAGGAGCTGGGCCGCTGGRACGCTCTGGTGGTCATGTYTGGA 312

Qy         81 AspGlyLeuMetHisGluValValAsnGlyLeu-MetGluArgProAspTrpGluThrAl 100
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        313 GACGGGCTGATGCACGAGGTGGTGAACGGGCTTCATGGAGCGGCCTGACTGGGAGACCGC 372

Qy        100 aIleGlnLysProLeuCysSerLeuProAlaGlySerGlyAsnAlaLeuAlaAlaSerLe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        373 CATCCAGAAGCCCCTGTGTAGCCTCCCAGCAGGCTCTGGCAACGCSCTGGCAGCTTCCTT 432

Qy        120 uAsnHisTyrAlaGlyTyrGluGlnValThrAsnGluAspLeuLeuThrAsnCysThrLe 140
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        433 RAACCATTATGCTGGCTATRAGCAGGTCACCAATGAAGACCTCCTGACCAACTGCACGCT 492

Qy        140 uLeuLeuCysArgProValLeuSerProMetAsnLeuLeuSerLeuHisThrAlaSerGl 160
              |||||||||||||  :::||||||||||||||||||||||||||||||||||||||||||
Db        493 ATTGCTGTGCCGCCGGCTGCTGTCACCCATGAACCTGCTGTCTCTGCACACGGCTTCGGG 552

Qy        160 yLeuArgSerPheSerValLeuSerLeuAlaTrpGlyPheIleAlaAspValAspLeuGl 180
              |||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        553 GCTGCGCCTCTTCTCTGTGCTCAGCCTGGCCTGGGGCTTCATTGCTGATGTGGACCTAGA 612

Qy        180 uSerAspLysTyrArgArgLeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgLe 200
              ||||:::||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        613 GAGTGAGAAGTATCGGCGTCTGGGGGAGATGCGCTTCACTCTGGGCACCTTCCTGCGTCT 672

Qy        200 uAlaAlaLeuArgThrTyrArgGlyArgLeuAlaThrLeuProValGlyArgValGlyPh 220
              ||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db        673 GGCAGCCCTGCGCACCTACCGCGGCCGACTGGCCTACCTCCCTGTAGGAAGAGTGGGTTC 732

Qy        220 eLysThrProAlaSerProValValValGlnGlnGlyProValAspAlaHisLeuValPr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        733 CAAGACACCTGCCTCCCCCGTTGTGGTCCAGCAGGGCCCGGTAGATGCACACCTTGTGCC 792

Qy        240 oLeuGluGluGlnValProSerHisTrpGlnValValProAspGluAspPheValLeuVa 260
              |||||||||  ||||||||||||||  ||||||||||||||||||||||||||||||||
Db        793 ACTGGAGGAGCCAGTGCCCTCTCACTGGACAGTGGTGCCCGACGAGGACTTTGTGCTAGT 852

Qy        260 lLeuAlaLeuLeuHisSerHisLeuAlaSerGluMetPheAlaAlaProMetGlyArgCy 280
              ||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||
Db        853 CCTGGCACTGCTGCACTCGCACCTGGGCAGTGAGATGTTTGCTGCACCCATGGGCCGCTG 912

Qy        280 sAlaAlaGlyValMetHisLeuPheTyrValArgAlaGlyValSerArgAlaMetLeuLe 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        913 TGCAGCTGGCGTCATGCATCTGTTCTACGTGCGGGCGGGAGTGTCTCGTGCCATGCTGCT 972

Qy        300 uArgLeuPheLeuAlaMetGluLysGlyArgHisMetGluTyrGluCysProTyrLeuVa 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        973 GCGCCTCTTCCTGGCCATGGAGAAGGGCAGGCATATGGAGTATGAATGCCCCTACTTGGT 1032

Qy        320 lTyrValProValValAlaPheArgLeuGluProLysAspGlyLysGlyValPheAlaVa 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1033 ATATGTGCCCGTGGTCGCCTTCCGCTTGGAGCCCAAGGATGGGAAAGGTGTGTTTGCAGT 1092

Qy        340 lAspGlyGluLeuMetValSerGluAlaValGlnGlyGlnValHisProAsnTyrPheTr 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1093 GGATGGGGAATTGATGGTTAGCGAGGCCGTGCAGGGCCAGGTGCACCCAAACTACTTCTG 1152

Qy        360 pMetValSerGlyCysValGluProProProSerTrpLysProGlnGlnMetProProPr 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1153 GATGGTCAGCGGTTGCGTGGAGCCCCCGCCCAGCTGGAAGCCCCAGCAGATGCCACCGCC 1212

Qy        380 oGluGluProLeu 384
              |||||||||||||
Db       1213 AGAAGAGCCCTTA 1225

RESULT 10
US-10-004-860-90
; Sequence 90, Application US/10004860
; Publication No. US20030065160A1
; GENERAL INFORMATION:
```

```
;  APPLICANT: Young et al.
;  TITLE OF INVENTION: 207 Human Secreted Proteins
;  FILE REFERENCE: PZ007P1
;  CURRENT APPLICATION NUMBER: US/10/004,860
;  CURRENT FILING DATE:  2001-12-07
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 1227
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (12)
;   OTHER INFORMATION: n equals a,t,g, or c
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (123)
;   OTHER INFORMATION: n equals a,t,g, or c
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1522)
;   OTHER INFORMATION: n equals a,t,g, or c
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1527)
;   OTHER INFORMATION: n equals a,t,g, or c
US-10-004-860-90

Alignment Scores:
Pred. No.:                1.58e-235      Length:          1533
Score:                    1927.00        Matches:         371
Percent Similarity:       96.88%         Conservative:    2
Best Local Similarity:    96.36%         Mismatches:      11
Query Match:              95.63%         Indels:          1
DB:                       13             Gaps:            0

US-09-784-810C-2 (1-384) x US-10-004-860-90 (1-1533)

Qy          1 MetAspProAlaGlyGlyProArgGlyValLeuProArgProCysArgValLeuValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||  |||||||||
Db         73 ATGGATCCAGCGGGCGGCCCCCGGGGCGTGCTCCCGCGGCCCTGCCGGTGNCTGGTGCTG 132

Qy         21 LeuAsnProArgGlyGlyLysGlyLysAlaLeuGlnLeuPheArgSerHisValGlnPro 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        133 CTGAACCCGCGCGGCGGCAAGGGCAAGGCCTTGCAGCTCTTCCGGAGTCACGTGCAGCCC 192

Qy         41 LeuLeuAlaGluAlaGluIleSerPheThrLeuMetLeuThrGluArgArgAsnHisAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 CTTTTGGCTGAGGCTGAAATCTCCTTCACGCTGATGCTCACTGAGCGGCGGAACCACGCG 252

Qy         61 ArgGluLeuValArgSerGluGluLeuGlyArgTrpAspAlaLeuValValMetSerGly 80
              ||||||||||||||||||||||||||||||||||  ||||||||||||||||  |||
Db        253 CGGGARCTGGTGCGGTCGGAGGAGCTGGGCCGCTGGRACGCTCTGGTGGTCATGTYTGGA 312

Qy         81 AspGlyLeuMetHisGluValValAsnGlyLeu-MetGluArgProAspTrpGluThrAl 100
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        313 GACGGGCTGATGCACGAGGTGGTGAACGGGCTTCATGGAGCGGCCTGACTGGGAGACCGC 372

Qy        100 aIleGlnLysProLeuCysSerLeuProAlaGlySerGlyAsnAlaLeuAlaAlaSerLe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        373 CATCCAGAAGCCCCTGTGTAGCCTCCCAGCAGGCTCTGGCAACGCSCTGGCAGCTTCCTT 432

Qy        120 uAsnHisTyrAlaGlyTyrGluGlnValThrAsnGluAspLeuLeuThrAsnCysThrLe 140
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db        433 RAACCATTATGCTGGCTATRAGCAGGTCACCAATGAAGACCTCCTGACCAACTGCACGCT 492

Qy        140 uLeuLeuCysArgProValLeuSerProMetAsnLeuLeuSerLeuHisThrAlaSerGl 160
              |||||||||||||  :::||||||||||||||||||||||||||||||||||||||||||||
Db        493 ATTGCTGTGCCGCCGGCTGCTGTCACCCATGAACCTGCTGTCTCTGCACACGGCTTCGGG 552

Qy        160 yLeuArgSerPheSerValLeuSerLeuAlaTrpGlyPheIleAlaAspValAspLeuGl 180
              |||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        553 GCTGCGCCTCTTCTCTGTGCTCAGCCTGGCCTGGGGCTTCATTGCTGATGTGGACCTAGA 612

Qy        180 uSerAspLysTyrArgArgLeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgLe 200
              ||||:::||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        613 GAGTGAGAAGTATCGGCGTCTGGGGGAGATGCGCTTCACTCTGGGCACCTTCCTGCGTCT 672

Qy        200 uAlaAlaLeuArgThrTyrArgGlyArgLeuAlaThrLeuProValGlyArgValGlyPh 220
              ||||||||||||||||||||||||||||||||||  |||||||||||||||||||||||
Db        673 GGCAGCCCTGCGCACCTACCGCGGCCGACTGGCCTACCTCCCTGTAGGAAGAGTGGGTTC 732

Qy        220 eLysThrProAlaSerProValValValGlnGlnGlyProValAspAlaHisLeuValPr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        733 CAAGACACCTGCCTCCCCCGTTGTGGTCCAGCAGGGCCCGGTAGATGCACACCTTGTGCC 792

Qy        240 oLeuGluGluGlnValProSerHisTrpGlnValValProAspGluAspPheValLeuVa 260
              ||||||||||  ||||||||||||||||  ||||||||||||||||||||||||||||||
Db        793 ACTGGAGGAGCCAGTGCCCTCTCACTGGACAGTGGTGCCCGACGAGGACTTTGTGCTAGT 852

Qy        260 lLeuAlaLeuLeuHisSerHisLeuAlaSerGluMetPheAlaAlaProMetGlyArgCy 280
              ||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||
Db        853 CCTGGCACTGCTGCACTCGCACCTGGGCAGTGAGATGTTTGCTGCACCCATGGGCCGCTG 912

Qy        280 sAlaAlaGlyValMetHisLeuPheTyrValArgAlaGlyValSerArgAlaMetLeuLe 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        913 TGCAGCTGGCGTCATGCATCTGTTCTACGTGCGGGCGGGAGTGTCTCGTGCCATGCTGCT 972

Qy        300 uArgLeuPheLeuAlaMetGluLysGlyArgHisMetGluTyrGluCysProTyrLeuVa 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        973 GCGCCTCTTCCTGGCCATGGAGAAGGGCAGGCATATGGAGTATGAATGCCCCTACTTGGT 1032

Qy        320 lTyrValProValValAlaPheArgLeuGluProLysAspGlyLysGlyValPheAlaVa 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1033 ATATGTGCCCGTGGTCGCCTTCCGCTTGGAGCCCAAGGATGGGAAAGGTGTGTTTGCAGT 1092

Qy        340 lAspGlyGluLeuMetValSerGluAlaValGlnGlyGlnValHisProAsnTyrPheTr 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1093 GGATGGGGAATTGATGGTTAGCGAGGCCGTGCAGGGCCAGGTGCACCCAAACTACTTCTG 1152

Qy        360 pMetValSerGlyCysValGluProProProSerTrpLysProGlnGlnMetProProPr 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1153 GATGGTCAGCGGTTGCGTGGAGCCCCCGCCCAGCTGGAAGCCCCAGCAGATGCCACCGCC 1212

Qy        380 oGluGluProLeu 384
              |||||||||||||
Db       1213 AGAAGAGCCCTTA 1225

RESULT 11
US-10-023-282-90
; Sequence 90, Application US/10023282
; Publication No. US20030092893A1
; GENERAL INFORMATION:
;  APPLICANT: Young et al.
;  TITLE OF INVENTION: 207 Human Secreted Proteins
;  FILE REFERENCE: PZ007P1
;  CURRENT APPLICATION NUMBER: US/10/023,282
;  CURRENT FILING DATE: 2001-12-20
;  EARLIER APPLICATION NUMBER: 09/205,258
;  EARLIER FILING DATE: 1998-12-04
;  EARLIER APPLICATION NUMBER: PCT/US98/11422
;  EARLIER FILING DATE: 1998-06-04
;  EARLIER APPLICATION NUMBER: 60/048,885
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/049,375
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,881
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,880
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,896
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/049,020
;  EARLIER FILING DATE: 1997-06-06
```

; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (12)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (123)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1522)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1527)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-023-282-90

Alignment Scores:

Pred. No.:	1.58e-235	Length:	1533
Score:	1927.00	Matches:	371
Percent Similarity:	96.88%	Conservative:	2
Best Local Similarity:	96.36%	Mismatches:	11
Query Match:	95.63%	Indels:	1
DB:	15	Gaps:	0

US-09-784-810C-2 (1-384) x US-10-023-282-90 (1-1533)

```
Qy          1 MetAspProAlaGlyGlyProArgGlyValLeuProArgProCysArgValLeuValLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         73 ATGGATCCAGCGGGCGGCCCCCGGGGCGTGCTCCCGCGGCCCTGCCGGTGNCTGGTGCTG 132

Qy         21 LeuAsnProArgGlyGlyLysGlyLysAlaLeuGlnLeuPheArgSerHisValGlnPro 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        133 CTGAACCCGCGCGGCGGCAAGGGCAAGGCCTTGCAGCTCTTCCGGAGTCACGTGCAGCCC 192

Qy         41 LeuLeuAlaGluAlaGluIleSerPheThrLeuMetLeuThrGluArgArgAsnHisAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 CTTTTGGCTGAGGCTGAAATCTCCTTCACGCTGATGCTCACTGAGCGGCGGAACCACGCG 252

Qy         61 ArgGluLeuValArgSerGluGluLeuGlyArgTrpAspAlaLeuValValMetSerGly 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 CGGGARCTGGTGCGGTCGGAGGAGCTGGGCCGCTGGRACGCTCTGGTGGTCATGTYTGGA 312

Qy         81 AspGlyLeuMetHisGluValValAsnGlyLeu-MetGluArgProAspTrpGluThrAl 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        313 GACGGGCTGATGCACGAGGTGGTGAACGGGCTTCATGGAGCGGCCTGACTGGGAGACCGC 372

Qy        100 aIleGlnLysProLeuCysSerLeuProAlaGlySerGlyAsnAlaLeuAlaAlaSerLe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        373 CATCCAGAAGCCCCTGTGTAGCCTCCCAGCAGGCTCTGGCAACGCSCTGGCAGCTTCCTT 432

Qy        120 uAsnHisTyrAlaGlyTyrGluGlnValThrAsnGluAspLeuLeuThrAsnCysThrLe 140
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db        433 RAACCATTATGCTGGCTATRAGCAGGTCACCAATGAAGACCTCCTGACCAACTGCACGCT 492

Qy        140 uLeuLeuCysArgProValLeuSerProMetAsnLeuLeuSerLeuHisThrAlaSerGl 160
              ||||||||||||  :::||||||||||||||||||||||||||||||||||||||||||||||
Db        493 ATTGCTGTGCCGCCGGCTGCTGTCACCCATGAACCTGCTGTCTCTGCACACGGCTTCGGG 552

Qy        160 yLeuArgSerPheSerValLeuSerLeuAlaTrpGlyPheIleAlaAspValAspLeuGl 180
              |||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        553 GCTGCGCCTCTTCTCTGTGCTCAGCCTGGCCTGGGGCTTCATTGCTGATGTGGACCTAGA 612

Qy        180 uSerAspLysTyrArgArgLeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgLe 200
              ||||:::||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        613 GAGTGAGAAGTATCGGCGTCTGGGGGAGATGCGCTTCACTCTGGGCACCTTCCTGCGTCT 672

Qy        200 uAlaAlaLeuArgThrTyrArgGlyArgLeuAlaThrLeuProValGlyArgValGlyPh 220
              ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        673 GGCAGCCCTGCGCACCTACCGCGGCCGACTGGCCTACCTCCCTGTAGGAAGAGTGGGTTC 732

Qy        220 eLysThrProAlaSerProValValValGlnGlnGlyProValAspAlaHisLeuValPr 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

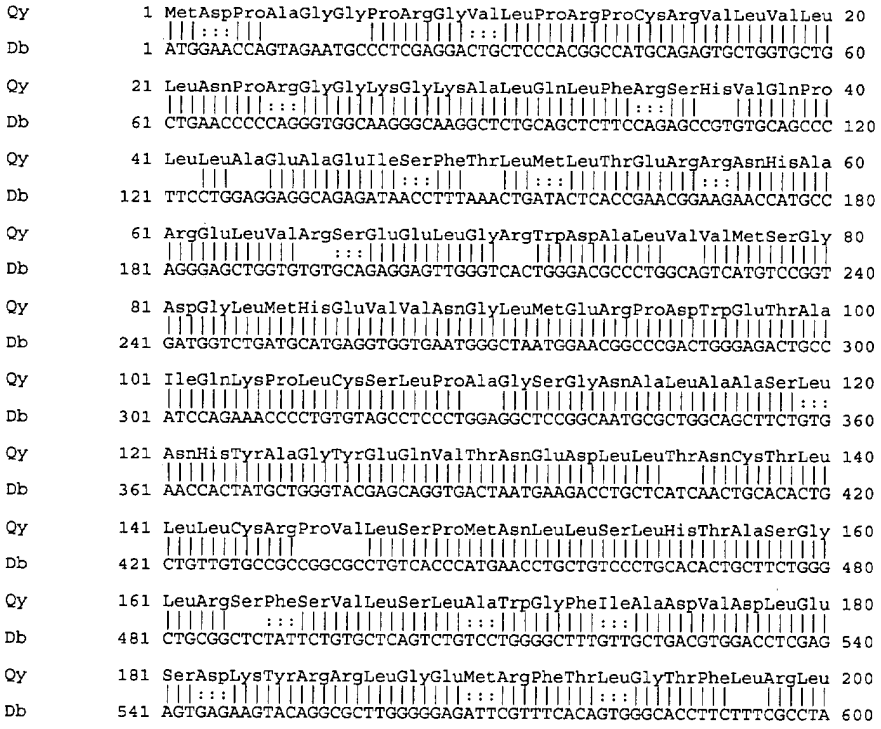
```
Db        733 CAAGACACCTGCCTCCCCCGTTGTGGTCCAGCAGGGCCCGGTAGATGCACACCTTGTGCC 792

Qy        240 oLeuGluGluGlnValProSerHisTrpGlnValValProAspGluAspPheValLeuVa 260

Db        793 ACTGGAGGAGCCAGTGCCCTCTCACTGGACAGTGGTGCCCGACGAGGACTTTGTGCTAGT 852

Qy        260 lLeuAlaLeuLeuHisSerHisLeuAlaSerGluMetPheAlaAlaProMetGlyArgCy 280

Db        853 CCTGGCACTGCTGCACTCGCACCTGGGCAGTGAGATGTTTGCTGCACCCATGGGCCGCTG 912

Qy        280 sAlaAlaGlyValMetHisLeuPheTyrValArgAlaGlyValSerArgAlaMetLeuLe 300

Db        913 TGCAGCTGGCGTCATGCATCTGTTCTACGTGCGGGCGGGAGTGTCTCGTGCCATGCTGCT 972

Qy        300 uArgLeuPheLeuAlaMetGluLysGlyArgHisMetGluTyrGluCysProTyrLeuVa 320

Db        973 GCGCCTCTTCCTGGCCATGGAGAAGGGCAGGCATATGGAGTATGAATGCCCCTACTTGGT 1032

Qy        320 lTyrValProValValAlaPheArgLeuGluProLysAspGlyLysGlyValPheAlaVa 340

Db       1033 ATATGTGCCCGTGGTCGCCTTCCGCTTGGAGCCCAAGGATGGGAAAGGTGTGTTTGCAGT 1092

Qy        340 lAspGlyGluLeuMetValSerGluAlaValGlnGlyGlnValHisProAsnTyrPheTr 360

Db       1093 GGATGGGGAATTGATGGTTAGCGAGGCCGTGCAGGGCCAGGTGCACCCAAACTACTTCTG 1152

Qy        360 pMetValSerGlyCysValGluProProProSerTrpLysProGlnGlnMetProProPr 380

Db       1153 GATGGTCAGCGGTTGCGTGGAGCCCCCGCCCAGCTGGAAGCCCCAGCAGATGCCACCGCC 1212

Qy        380 oGluGluProLeu 384

Db       1213 AGAAGAGCCCTTA 1225

RESULT 12
US-09-784-810A-3
; Sequence 3, Application US/09784810A
; Patent No. US20020082203A1
; GENERAL INFORMATION:
;  APPLICANT: RASTELLI, LUCA
;  TITLE OF INVENTION: NOVEL SPHINGOSINE KINASES AND NUCLEIC ACIDS ENCODING
;  TITLE OF INVENTION:  SAME
;  FILE REFERENCE: 10716-08
;  CURRENT APPLICATION NUMBER: US/09/784,810A
;  CURRENT FILING DATE:  2001-02-14
;  PRIOR APPLICATION NUMBER: 60/182,360
;  PRIOR FILING DATE: 2000-02-14
;  PRIOR APPLICATION NUMBER: 60/191,261
;  PRIOR FILING DATE: 2000-03-22
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 1759
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-784-810A-3

Alignment Scores:
Pred. No.:              6.2e-193        Length:         1759
Score:                  1594.50         Matches:        303
Percent Similarity:     88.25%          Conservative:   35
Best Local Similarity:  79.11%          Mismatches:     44
Query Match:            79.13%          Indels:         1
DB:                     9               Gaps:           1

US-09-784-810C-2 (1-384) x US-09-784-810A-3 (1-1759)

Qy          1 MetAspProAlaGlyGlyProArgGlyValLeuProArgProCysArgValLeuValLeu 20

Db        327 ATGGAACCAGTAGAATGCCCTCGAGGACTGCTCCCACGGCCATGCAGAGTGCTGGTGCTG 386

Qy         21 LeuAsnProArgGlyGlyLysGlyLysAlaLeuGlnLeuPheArgSerHisValGlnPro 40

Db        387 CTGAACCCCCAGGGTGGCAAGGGCAAGGCTCTGCAGCTCTTCCAGAGCCGTGTGCAGCCC 446

Qy         41 LeuLeuAlaGluAlaGluIleSerPheThrLeuMetLeuThrGluArgArgAsnHisAla 60

Db        447 TTCCTGGAGGAGGCAGAGATAACCTTTAAACTGATACTCACCGAACGGAAGAACCATGCC 506

Qy         61 ArgGluLeuValArgSerGluGluLeuGlyArgTrpAspAlaLeuValValMetSerGly 80

Db        507 AGGGAGCTGGTGTGTGCAGAGGAGTTGGGTCACTGGGACGCCCTGGCAGTCATGTCCGGT 566

Qy         81 AspGlyLeuMetHisGluValValAsnGlyLeuMetGluArgProAspTrpGluThrAla 100

Db        567 GATGGTCTGATGCATGAAGTGGTGAATGGGCTAATGGAACGGCCAGACTGGGAGACTGCC 626

Qy        101 IleGlnLysProLeuCysSerLeuProAlaGlySerGlyAsnAlaLeuAlaAlaSerLeu 120

Db        627 ATCCAGAAACCCCTGTGTAGCCTCCCTGGAGGCTCCGGCAATGCGCTGGCAGCTTCTGTG 686

Qy        121 AsnHisTyrAlaGlyTyrGluGlnValThrAsnGluAspLeuLeuThrAsnCysThrLeu 140

Db        687 AACCACTATGCTGGGTACGAGCAGGTGACTAATGAAGACCTGCTCATCAACTGCACACTG 746

Qy        141 LeuLeuCysArgProValLeuSerProMetAsnLeuLeuSerLeuSerLeuHisThrAlaSerGly 160

Db        747 CTGTTGTGCCGCCGGCGCCTGTCACCCATGAACCTGCTGTCCCTGCACACTGCTTCTGGG 806

Qy        161 LeuArgSerPheSerValLeuSerLeuAlaTrpGlyPheIleAlaAspValAspLeuGlu 180

Db        807 CTGCGGCTCTATTCTGTGCTCAGTCTGTCCTGGGGCTTTGTTGCTGACGTGGACCTCGAG 866

Qy        181 SerAspLysTyrArgArgLeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgLeu 200

Db        867 AGTGAGAAGTACAGGCGCTTGGGGGAGATTCGTTTCACAGTGGGCACCTTCTTTCGCCTA 926

Qy        201 AlaAlaLeuArgThrTyrArgGlyArgLeuAlaThrLeuProValGlyArgValGlyPhe 220

Db        927 GCAAGCCTGCGCATCTACCAAGGCCAACTGGCCTACCTTCCTGTAGGAACTGTGGCCTCT 986

Qy        221 LysThrProAlaSerProValValValGlnGlnGlyProValAspAlaHisLeuValPro 240

Db        987 AAGAGACCCGCCTCT---ACACTGGTGCAGAAGGGCCCCGTCGACACACACCTTGTTCCT 1043

Qy        241 LeuGluGluGlnValProSerHisTrpGlnValValProAspGluAspPheValLeuVal 260

Db       1044 CTGGAGGAGCCAGTGCCTTCTCATTGGACTGTGGTACCAGAACAGGACTTCGTCCTGGTG 1103

Qy        261 LeuAlaLeuLeuHisSerHisLeuAlaSerGluMetPheAlaAlaProMetGlyArgCys 280

Db       1104 CTGGTGCTGCTACACACCCACCTGAGCTCCGAGCTGTTTGCAGCACCCATGGGCCGCTGT 1163

Qy        281 AlaAlaGlyValMetHisLeuPheTyrValArgAlaGlyValSerArgAlaMetLeuLeu 300

Db       1164 GAGGCTGGTGTTATGCATCTGTTCTACGTACGTGCGGGGGTGTCAAGGGCTGCGCTGCTG 1223

Qy        301 ArgLeuPheLeuAlaMetGluLysGlyArgHisMetGluTyrGluCysProTyrLeuVal 320

Db       1224 CGCCTCTTCCTGGCCATGCAGAAGGGCAAGCATATGGAACTTGACTGTCCATACCTGGTT 1283

Qy        321 TyrValProValValAlaPheArgLeuGluProLysAspGlyLysGlyValPheAlaVal 340

Db       1284 CATGTGCCCGTGGTTGCTTTCCGCCTGGAGCCCAGGAGCCAGAGGGGCGTGTTTTCTGTG 1343

Qy        341 AspGlyGluLeuMetValSerGluAlaValGlnGlyGlnValHisProAsnTyrPheTrp 360

Db       1344 GATGGAGAGCTGATGGTATGTGAAGCTGTGCAGGGCCAAGTGCACCCAAACTACCTTTGG 1403

Qy        361 MetValSerGlyCysValGluProProProSerTrpLysProGlnGlnMetProProPro 380

Db       1404 ATGGTCTGTGGCAGCAGAGATGCCCCATCCGGCCGGGACTCCCGGCGGGGGCCACCTCCA 1463

Qy        381 GluGluPro 383

Db       1464 GAAGAACCA 1472
```

RESULT 13
US-09-970-516-5
; Sequence 5, Application US/09970516
; Patent No. US20020099029A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020099029Alartis AG
; TITLE OF INVENTION: Induction of blood vessel formation through administration of
; TITLE OF INVENTION: polynucleotides encoding sphingosine kinases
; FILE REFERENCE: 4-31617
; CURRENT APPLICATION NUMBER: US/09/970,516
; CURRENT FILING DATE: 2001-10-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1149
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1149)
; OTHER INFORMATION:
US-09-970-516-5

Alignment Scores:

Pred. No.:	2.54e-192	Length:	1149
Score:	1587.50	Matches:	302
Percent Similarity:	87.99%	Conservative:	35
Best Local Similarity:	78.85%	Mismatches:	45
Query Match:	78.78%	Indels:	1
DB:	9	Gaps:	1

US-09-784-810C-2 (1-384) x US-09-970-516-5 (1-1149)

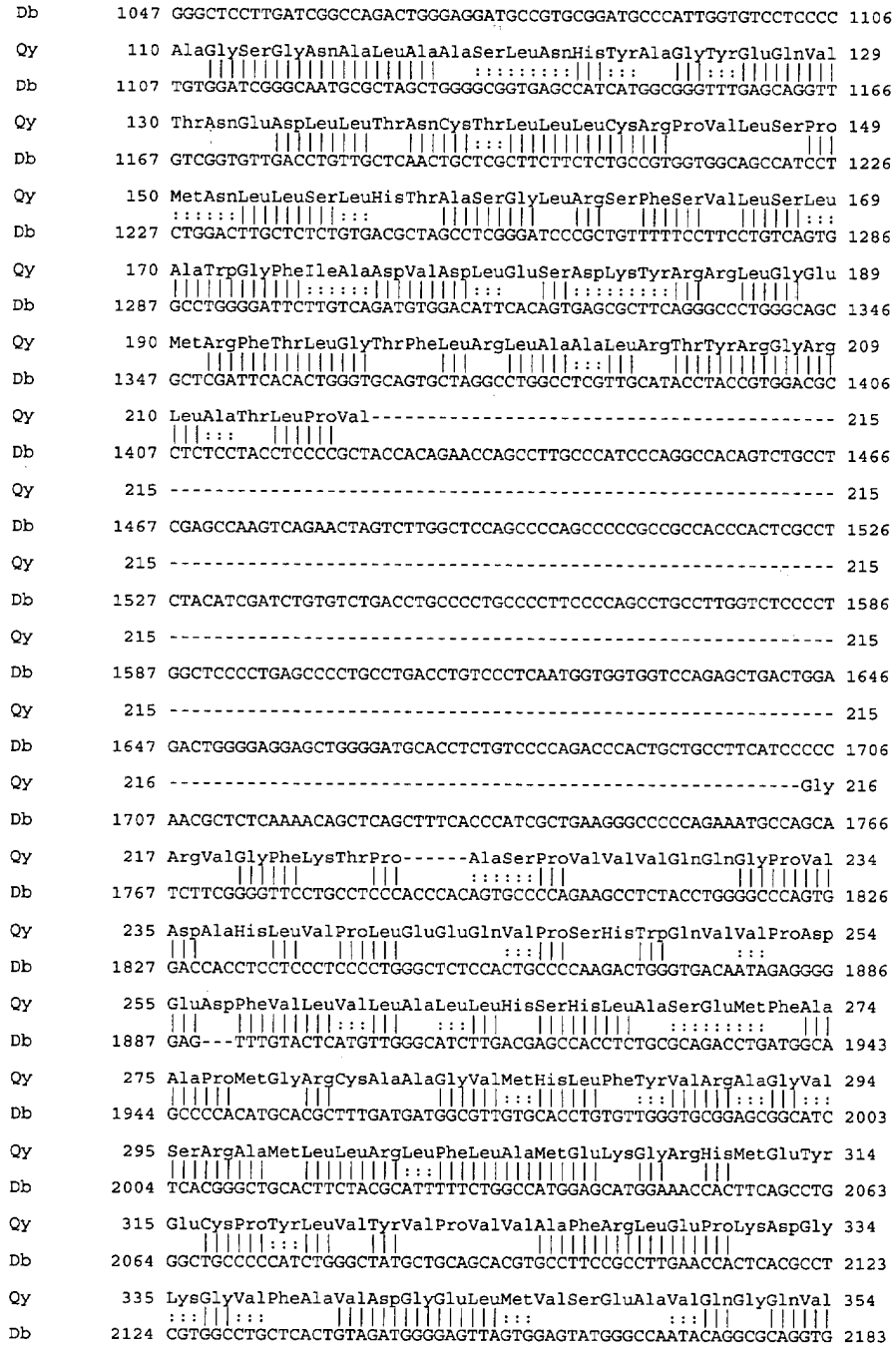


RESULT 14
US-10-619-344-5
; Sequence 5, Application US/10619344
; Publication No. US20040086487A1
; GENERAL INFORMATION:
; APPLICANT: Novartis AG
; TITLE OF INVENTION: Induction of blood vessel formation through administration of
; TITLE OF INVENTION: polynucleotides encoding sphingosine kinases
; FILE REFERENCE: 4-31617
; CURRENT APPLICATION NUMBER: US/10/619,344
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: US/09/970,516
; PRIOR FILING DATE: 2001-10-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1149
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1149)
; OTHER INFORMATION:
US-10-619-344-5

Alignment Scores:

Pred. No.:	2.54e-192	Length:	1149
Score:	1587.50	Matches:	302
Percent Similarity:	87.99%	Conservative:	35
Best Local Similarity:	78.85%	Mismatches:	45
Query Match:	78.78%	Indels:	1
DB:	17	Gaps:	1

```
US-09-784-810C-2 (1-384) x US-10-619-344-5 (1-1149)

Qy          1 MetAspProAlaGlyGlyProArgGlyValLeuProArgProCysArgValLeuValLeu 20
              |||:::|||     |||||||||:::|||||||||||||||||||||||||||||||||
Db          1 ATGGAACCAGTAGAATGCCCTCGAGGACTGCTCCCACGGCCATGCAGAGTGCTGGTGCTG 60

Qy         21 LeuAsnProArgGlyGlyLysGlyLysAlaLeuGlnLeuPheArgSerHisValGlnPro 40
              |||||||||:::|||||||||||||||||||||||||||||:::|||   |||||||||
Db         61 CTGAACCCCCAGGGTGGCAAGGGCAAGGCTCTGCAGCTCTTCCAGAGCCGTGTGCAGCCC 120

Qy         41 LeuLeuAlaGluAlaGluIleSerPheThrLeuMetLeuThrGluArgArgAsnHisAla 60
                 |||   |||||||||||||:::|||   |||:::|||||||||||||:::|||||||||
Db        121 TTCCTGGAGGAGGCAGAGATAACCTTTAAACTGATACTCACCGAACGGAAGAACCATGCC 180

Qy         61 ArgGluLeuValArgSerGluGluLeuGlyArgTrpAspAlaLeuValValMetSerGly 80
              ||||||||||||   :::|||||||||||||   ||||||||||||   ||||||||||||
Db        181 AGGGAGCTGGTGTGTGCAGAGGAGTTGGGTCACTGGGACGCCCTGGCAGTCATGTCCGGT 240

Qy         81 AspGlyLeuMetHisGluValValAsnGlyLeuMetGluArgProAspTrpGluThrAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GATGGTCTGATGCATGAGGTGGTGAATGGGCTAATGGAACGGCCCGACTGGGAGACTGCC 300

Qy        101 IleGlnLysProLeuCysSerLeuProAlaGlySerGlyAsnAlaLeuAlaAlaSerLeu 120
              |||||||||||||||||||||||||   |||||||||||||||||||||||||:::
Db        301 ATCCAGAAACCCCTGTGTAGCCTCCCTGGAGGCTCCGGCAATGCGCTGGCAGCTTCTGTG 360

Qy        121 AsnHisTyrAlaGlyTyrGluGlnValThrAsnGluAspLeuLeuThrAsnCysThrLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||
Db        361 AACCACTATGCTGGGTACGAGCAGGTGACTAATGAAGACCTGCTCATCAACTGCACACTG 420

Qy        141 LeuLeuCysArgProValLeuSerProMetAsnLeuLeuSerLeuHisThrAlaSerGly 160
              ||||||||||||      ||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGTTGTGCCGCCGGCGCCTGTCACCCATGAACCTGCTGTCCCTGCACACTGCTTCTGGG 480

Qy        161 LeuArgSerPheSerValLeuSerLeuAlaTrpGlyPheIleAlaAspValAspLeuGlu 180
              ||||||   :::|||||||||||||||:::|||||||||:::|||||||||||||||||
Db        481 CTGCGGCTCTATTCTGTGCTCAGTCTGTCCTGGGGCTTTGTTGCTGACGTGGACCTCGAG 540

Qy        181 SerAspLysTyrArgArgLeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgLeu 200
              |||:::|||||||||||||||||||:::|||||||||:::|||||||||   ||||||
Db        541 AGTGAGAAGTACAGGCGCTTGGGGGAGATTCGTTTCACAGTGGGCACCTTCTTTCGCCTA 600

Qy        201 AlaAlaLeuArgThrTyrArgGlyArgLeuAlaThrLeuProValGlyArgValGlyPhe 220
              |||:::||||||   |||:::|||:::||||||   ||||||||||||   |||
Db        601 GCAAGCCTGCGCATCTACCAAGGCCAACTGGCCTACCTTCCTGTAGGAACTGTGGCCTCT 660

Qy        221 LysThrProAlaSerProValValValGlnGlnGlyProValAspAlaHisLeuValPro 240
              |||   |||||||||      :::|||||||:::||||||||||||   ||||||||||||
Db        661 AAGAGACCCGCCTCT---ACACTGGTGCAGAAGGGCCCCGTCGACACACACCTTGTTCCT 717

Qy        241 LeuGluGluGlnValProSerHisTrpGlnValValProAspGluAspPheValLeuVal 260
              |||||||||   ||||||||||||||||   |||||||||:::::|||||||||||||||
Db        718 CTGGAGGAGCCAGTGCCTTCTCATTGGACTGTGGTACCAGAACAGGACTTTGTCCTGGTG 777

Qy        261 LeuAlaLeuLeuHisSerHisLeuAlaSerGluMetPheAlaAlaProMetGlyArgCys 280
              |||   |||||||||:::||||||:::||||||:::||||||||||||||||||||||||
Db        778 CTGGTGCTGCTACACACCCACCTGAGCTCCGAGCTGTTTGCAGCACCCATGGGCCGCTGT 837

Qy        281 AlaAlaGlyValMetHisLeuPheTyrValArgAlaGlyValSerArgAlaMetLeuLeu 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        838 GAGGCTGGTGTTATGCATCTGTTCTACGTACGTGCGGGGGTGTCAAGGGCTGCGCTGCTG 897

Qy        301 ArgLeuPheLeuAlaMetGluLysGlyArgHisMetGluTyrGluCysProTyrLeuVal 320
              ||||||||||||||||||:::||||||:::||||||||   :::||||||||||||||||
Db        898 CGCCTCTTCCTGGCCATGCAGAAGGGCAAGCATATGGAACTTGACTGTCCATACCTGGTT 957

Qy        321 TyrValProValValAlaPheArgLeuGluProLysAspGlyLysGlyValPheAlaVal 340
              :::|||||||||||||||||||||||||||||:::      :::||||||||:::|||
Db        958 CATGTGCCCGTGGTTGCTTTCCGCCTGGAGCCCAGGAGCCAGAGGGGCGTGTTTTCTGTG 1017

Qy        341 AspGlyGluLeuMetValSerGluAlaValGlnGlyGlnValHisProAsnTyrPheTrp 360
              ||||||   |||||||||   |||||||||||||||||||||||||||||||   |||

Db        1018 GATGGAGGGCTGATGGTATGTGAAGCTGTGCAGGGCCAAGTGCACCCAAACTACCTTTGG 1077

Qy         361 MetValSerGlyCysValGluProProProSerTrpLysProGlnGlnMetProProPro 380
               ||||||   |||      :::   |||                :::::   |||||||||
Db        1078 ATGGTCTGTGGCAGCAGAGATGCCCCATCCGGCCGGGACTCCCGGCGGGGGCCACCTCCA 1137

Qy         381 GluGluPro 383
               |||||||||
Db        1138 GAAGAACCA 1146

RESULT 15
US-09-817-676A-11
; Sequence 11, Application US/09817676A
; Patent No. US20020042101A1
; GENERAL INFORMATION:
;  APPLICANT: Spiegel, Sarah
;  APPLICANT:  Kohama, Takafumi
;  TITLE OF INVENTION: Mammalian Sphingosine Kinase Type 2 Isoforms, Cloning,
;  TITLE OF INVENTION:  Expression and Methods of Use Thereof
;  FILE REFERENCE: 00170/HG
;  CURRENT APPLICATION NUMBER: US/09/817,676A
;  CURRENT FILING DATE:  2001-03-26
;  PRIOR APPLICATION NUMBER: US 60/194,318
;  PRIOR FILING DATE: 2000-04-03
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
;   LENGTH: 2698
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (387)..(2237)
;  PUBLICATION INFORMATION:
;   TITLE: Molecular cloning and functional characterization of a
;   TITLE: novel mammalian sphingosine kinase type 2 isoform
;   JOURNAL: J. Biol. Chem.
;   VOLUME: 275
;   ISSUE: 26
;   PAGES: 19513-19520
;   DATE: 2000-06-30
;   DATABASE ACCESSION NUMBER: AF245448
;   DATABASE ENTRY DATE: 2000-06-27
US-09-817-676A-11

Alignment Scores:
Pred. No.:                1.11e-100       Length:          2698
Score:                    875.00          Matches:         187
Percent Similarity:       51.98%          Conservative:    63
Best Local Similarity:    38.88%          Mismatches:      111
Query Match:              43.42%          Indels:          120
DB:                       9               Gaps:            4

US-09-784-810C-2 (1-384) x US-09-817-676A-11 (1-2698)

Qy          10 ValLeuProArgProCysArgValLeuValLeuLeuAsnProArgGlyGlyLysGlyLys 29
               :::|||||||||      |||:::|||:::|||:::||||||   ||||||:::|||
Db         807 TTGCTGCCCCCGGAAGCCCAGGCTGCTCATATTGGTCAATCCCTTTGGGGGGCGGGGCCTG 866

Qy          30 AlaLeuGlnLeuPheArgSerHisValGlnProLeuLeuAlaGluAlaGluIleSerPhe 49
               |||   |||             ||||||   |||:::::::::||||||   :::|||||||
Db         867 GCCTGGCAGCGCTGTATGGACCACGTGGTGCCAATGATCTCTGAAGCTGGGCTGTCCTTC 926

Qy          50 ThrLeuMetLeuThrGluArgArgAsnHisAlaArgGluLeuValArgSerGluGluLeu 69
               |||:::   ||||||||:::|||||||||||||||||||:::          |||
Db         927 AACCTCATACAGACAGAACGACAGAACCATGCCCGTGAGCTGGTGCAGGGGTTAAGCCTG 986

Qy          70 GlyArgTrpAspAlaLeuValValMetSerGlyAspGlyLeuMetHisGluValValAsn 89
                  |||:::   :::|||   :::|||||||||||||:::::||||||:::|||
Db         987 AGTGAGTGGGAAGGCATTGTCACTGTGTCTGGAGACGGGCTGCTTTACGAGGTGCTGAAT 1046

Qy          90 GlyLeuMetGluArgProAspTrpGluThrAlaIleGlnLysProLeuCysSerLeuPro 109
               ||||||::::::|||||||||||||||   |||::::::   |||:::      ||||||
```



Search completed: August 20, 2004, 02:19:18
Job time : 614 secs